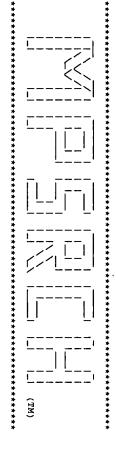
東



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Fri Jun 12 11:49:45 1998; MasPar time 24.12 Seconds 529.654 Million cell updates/sec

Title: >US-08-083-590A-2 (1-833) from USO8083590A.pep (1 of 2)

Description: Perfect Score Sequence: Score: 1 MHWIKCLLTAFICFTVIVQV......GSGAGTAQQQRSVVCGTPHM 833

Scoring table: PAM 150 Gap 11

124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 36.728; Variance 180.698; scale 0.203

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| \$\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\ | Result No. |
|--|----------------|
| 6143 1910 1910 1861 1839 1839 1826 1784 1778 1692 1692 1692 1693 1693 1693 1693 1693 1693 1693 1693 | Score |
| 31.0 31.0 30.2 29.8 29.6 29.6 29.6 27.4 27.2 27.2 27.3 27.3 21.8 21.8 21.8 21.8 21.8 21.8 21.8 21.8 | Query Match |
| 833 6 740 21 740 21 723 25 520 25 702 25 702 27 702 21 1236 19 1218 19 1218 25 1218 25 1228 25 1238 25 1238 25 1238 25 1248 25 1257 19 1257 19 | Length DB |
| 6 R28960 11 W00876 5 W18353 5 W18349 5 W18349 7 R38305 7 R38305 9 W05833 5 W18354 5 W18354 1 W11720 7 R38305 7 R38305 7 R38305 | B ID |
| Delta D11 C-Delta-1 polypeptide C-Delta-1 polypeptide C-Delta-1 polypeptide Proliferation and dif Proliferation and dif Proliferation and dif Proliferation and dif M-Delta-1 polypeptide Sequence of a delta p Chick Serrate- Human Serrate-1 (HJ1) Proliferation and dif Human Serrate-2 (HJ2) Sequence of a serrate H-Delta-1 polypeptide Proliferation and dif Adhesive protein. | Description |
| ptide 9.55e-151 ptide 9.95e-151 d dif 1.78e-146 d dif 1.44e-144 d dif 1.94e-143 lta p 8.50e-140 1.46e-134 (HJ1) 7.98e-132 d dif 8.74e-131 d dif 1.94e-130 d dif 1.94e-130 d dif 1.94e-130 d dif 1.94e-130 d dif 1.94e-130 d dif 2.42e-94 ptide 3.14e-62 ptide 3.14e-62 ptide 3.14e-62 d dif 5.31e-49 d dif 5.31e-49 | Pred. No. |

Query Match Best Local S Matches 83

ch 99.7%; l Similarity 99.8%; 831; Conservative

Score 6143; DB 6; Length 833; Pred. No. 0.00e+00; 0; Mismatches 2; Indels

0

Gaps

0;

| ./ 383 10 R56166 Neuroendocrine .5 1480 5 R25079 Drosophila SLIT .9 660 21 W11725 H-Delta-1 polyp .9 157 21 W11730 H-Delta-1 polyp .9 157 21 W1350 .8 192 25 W18350 Proliferation a .4 293 6 R28961 Serrate protein .0 2199 16 R94563 Chicken cytotact .6 1810 16 R94563 Antigen GX5401F .1 16 R94563 Antigen GX5401F .2 2189 1 R05222 Antigen GX5401F .1 751 10 R53088 Human masking p .1 751 10 R53086 Human masking p .1 752 10 R53086 Human masking p .1 753 10 R53086 Human masking p .1 754 10 R53089 Human masking p .1 755 10 R53080 Human masking p .1 756 10 R53080 Human masking p .1 757 10 R53080 Human masking p .1 758 10 R53080 Human masking p .1 759 10 R53080 Human masking p .1 759 BX2461 Masking protein .6 816 27 W37500 Human nel-relation .6 816 27 W37501 Human nel-relation .7 1257 9 R46627 Neurocan core p .7 1257 9 R46627 Neurocan core p .7 4544 11 R60517 Human alpha-2-M | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ა 5 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
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| | | | • | core | ELR-11 and -12. | receptor ME2 | nel-related | el-relate | 'n | beta 1 | mask | mask | masking | masking prote | | Mouse LTBP-3. | | Chicken cytotactin. | Human cytotactin. | Serrate protein. | Proliferation and dif | _ | polypeptic | T pro | | Neuroendocrine tumor |

ALIGNMENTS

| RESULT | LT 1 R28960 standard; Protein; 833 AA. |
|--------|---|
| S A | R28960; 01-APR-1993 (first entry) |
| Œ | Delta D11. |
| X | Human; Notch; plasmid; cDNA; clone; D11; expression library; PCR; |
| Z Z | polymerase chain reaction; primer; cloning vector; Delta; Serrate; |
| 2 2 | neurogenic; coporychmic; nomocypic; necerocypic; differenciacion; quantitation; antibody. |
| S | Homo sapiens. |
| NA | W09219734-A. |
| B | 12-NOV-1992. |
| PF | 01-MAY-1992; U03651. |
| PR | |
| PR | 1,166 |
| PA | (INDV) UNIV INDIANA FOUND. (UYYA) UNIV YALE. |
| ΡI | Artavanis-Tsakonas S, Blaumueller CM, Fehon RG, Muskavitch MAT; |
| ΙΫ́ | Rebay I, Shepard SB; wpr: 92-398861/48 |
| DR | N-PSDB; Q30997. |
| ΡT | Human Notch and Delta DNA and protein sequences - used for study |
| PΤ | and manipulation of differentiation processes |
| PS | Claim 50; Fig 13; 239pp; English. |
| င္ပ | The sequence given is encoded by the nucleotide sequence of human |
| ဂ | Delta gene contained in plasmid cDNA clone D11. A human expression |
| ဂ | library was constructed and screening assays were carried out on to |
| 유 | select for the expressed Delta product. Alternatively the sequences |
| င် | could be isolated by amplification using polymerase chain reaction |
| 8 | (PCR) primers. The isolated gene may be inserted into a cloning |
| 3 6 | vector and expressed. The Delta gene and also the Notch and Serrace |
| 3 6 | they encode are involved in specific home- or beterotypic interactions |
| ဂ | crucial to differentiation. The quantitation of mRNA for human Notch |
| ဂ | and Delta and adhesive molecules, and study of its expression are |
| င္ပ | possible using the DNA and antibodies raised against the Notch and |
| 8 | Delta proteins. |
| SQ | Sequence 833 AA; |

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/label- DSL
229..261
/label- EGF1
262..292
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28-APR-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 135pp; English.
C-delta-1 polypeptide (W11719) is the chick homologue of Drosophila Delta-1 polypeptide (W11719) is the chick homologue of Drosophila Delta-1 aprotein that binds to Notch protein. Expression of amino acid sequence was deduced from a cDNA clone (T58897) obtd. From chick stage 4-6 embryos. An alternatively spliced variant (W00876) was also isolated, and mouse (W11720) and human (W1171-38) Delta-1 polypeptides have been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, and nervous system disorders or to Sequence 727 AA;
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256 LCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRPCKNGGTCFNTGEGLX
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Best Local Similarity 50.1%; Pred. No. 9.95e-151;
Matches 263; Conservative 78; Mismatches 168;
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/label= EGF8
524..534
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/label- EGF7
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                   /label= EGF3
333..370
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555..579
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333.332
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28-JUN-1995; US-000589.
(IMCR ) IMPERIAL CANCER I
(UYYA ) UNIV YALE.
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regeneration
Siclosure; Fig 2; 135pp; English.
C delta-1 polypeptide (W00076) is the chick homologue of Drosophila
C delta-1 protein that binds to Notch protein. Expression of
C delta, a protein that binds to Notch protein. Expression of
C delta, a protein that binds to Notch protein. Expression of
C delta-1 correlates with onset of neurogenesis. The C-delta-1
C from chick stage 4-6 embryos. A shorter version (W58877) of
C delta-1, lacking the 12 C-terminal amino acids of the longer
C version, was also isolated, and mouse (W11720) and human (W11721-
C 38) Delta-1 polypeptides have been identified. Delta-1 proteins
C can be used to treat or prevent disorders characterised by
C increased Notch activity, such as cervical, breast, lung or colon
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28-JUN-1996; U11178.
28-JUN-1995; US-000589.
(IMCR ) IMPERIAL CANCER R
(UYYA ) UNIV YALE.
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C-Delta-1; cell proliferation; nervous system disorder;
tissue regeneration; Notch; cervix cancer; breast cance
lung cancer; colon cancer; melanoma; seminoma;
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28-APR-1997
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                                                              Claim 15;
                                                                                                   proliferation
                                                                                                                     Peptide(s)
                                                                                                                                                          (ASAH ) ASAHI KASEI KOGYO Itoh A, Sakano S; WPI; 97-298110/27.
                                                                                                                                                                                                                   15-NOV-1996; J03356.
30-NOV-1995; JP-311811.
17-NOV-1995; JP-299611.
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29-MAY-1997.
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                                                                                                                                                                                                               rcalalavlsallcqvwssgvfelklqefvnkkgllgnrnccrgga-gppp-c--acrtf 59
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prevention and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement blood formation, e.g. after immunosuppression.
                                                                                                                    Score 1861; DB 25; Length 723;
Pred. No. 1.78e-146;
86; Mismatches 171; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proliferation and differentiation suppression polypeptide. Proliferation; differentiation; suppression; human; delta-1; serrate-1; blood cell; neuron; leukaemia; malignant tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells, such as leukaemia and malignant rumouss
blood formation, e.g. after immunosuppression.
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Claim 3; Page 59-61; 114pp; Japanese.
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W18348 standard; protein; 520 i
W18348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-1997.
15-WOV-1996; J03356.
30-NOV-1995; JP-311811.
17-WOV-1995; JP-299611.
(ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                 ch 30.2%;
1 Similarity 48.4%;
261; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-1998 (first entry)
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WPI; 97-298110/27
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WO9719172-A1.
                                                                       Sequence
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Best Local
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                                                                                                                                                                                                                                                                                                                                    dafghftcgergekvcnpgwkgpyctepiclpgcdeghgfcdkpgeckcrvgwggrycde 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 APGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCHCANGWSGKMCEEKVLTCS 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dgpcfngg-r-c-sd-spdg-gyscrcpvgysgfncekkidycssspcsngakcvdlgda 405
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                                                                                                  1 sgvfelklqefvnkkgllgnrnccrgga-gppp-c--acrtffrvclkhyqasvspeppc 56
                                                                                                                                                    82
                                                      Gaps
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                                                                                                                                                                                                                                 SGSFELRLKYFSNDHGRDNBGRCCSGESDGATGKCLGSCKTRFRVCLKHYQATIDTTSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGC-E-HGHCDKPNQCVCQLGWKGALCNE
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Proliferation and differentiation suppression polypeptide.
Proliferation; differentiation; suppression; human; delta-1; serrate-1; blood cell; neuron; leukaemia; malignant tumour;
     Length 520;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506
                                                   80; Mismatches 164;
                               Pred. No. 1.44e-144;
     DB 25;
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     29.88;
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30-NOV-1995; JP-311811.
17-NOV-1995; JP-299611.
(ASAH ) ASAHI KASEI KOGYO
                         Similarity 49.1%;
256; Conservative
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WPI; 97-298110/2
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WO9719172-A1.
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                                         Claim 4; Fig 8; 135pp; English.

M-delta-1 polypeptide (W11720) is the mouse homologue of Drosophila Delta, a protein that binds to Notch protein. It is expressed primarily in presomitic mesoderm, the central and peripheral nervous systems, and kidney. Chick (W11719) and human (W11721-38) Delta-1 polypeptides have also been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon
                                                                                                                                                                                                                                                                  N-PSDB; T58899.
New vertebrate Delta protein, DNA preventing cancer, nervous system
                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M-Delta-1 polypeptide
M-Delta-1; cell proli
                        cancer, melanoma or seminoma, as well as nervous system
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28-JUN-1996; U11178.
28-JUN-1995; US-000589.
                                                                                                                                                                                                                                                                                                                                                                  Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue regeneration; Notch;
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       tissue
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    regeneration
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Mismatches 164;
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       and
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Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                          uelta protein;
brosophila melanogaster.
W09312141-A.
24-JUN-100-1
                                             extracellular domain. Molecular studies have lead to the suggestion that Notch and Delta constitute biochemically interacting elements of a cell communication mechanism involved in early developmental
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                                                                                                                 Delta encodes an approx. 100 kd protein (Delta denotes protein product of the predominant zygotic and maternal transcripts) that has nine EGF-like repeats within its
                                                                                                                                                                                    physiological processes
Disclosure; Page 85; 119pp;
                                                                                                                                                                                                              the study and manipulation physiological processes
                                                                                                                                                                                                                                 Purified serrate protein, nucleic the study and manipulation of diff
                                                                                                                                                                                                                                                                                N-PSDB; Q43911.
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WPI; 93-214095/26.
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11-DEC-1991;
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                          decisions
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larity 48.0%;
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Pred. No. 1.94e~143;
87; Mismatches 166;
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                                                                                                                                                                                                                                                           acid and antibodies
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Query Match Best Local

Similarity

28 100

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Score Pred.

1784; No. 8

DB 7; .50e-140;

Length

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Query Match 27.9%; Score 1718; DB 19;
Best Local Similarity 43.1%; Pred. No. 4.46e-134;
Matches 239; Conservative 103; Mismatches 184;
                                                                                                                                                                                                        Henrique DMP,
           854..911
/label= Cysteine-rich_region
1042..1066
/label= Transmembrane_domain
                                                                                           Intracellular_domain
                                                                                                                          12-SEP-1996.
07-MAR-1996.
07-MAR-1995. US-400159.
(IMCR.) IMPERIAL CANCER RES TECHNOLOGY.
(UYXA.) UNIV YALE.
                                                                                                                                                                                                 Artavanis-Tsakonas S, Gray GE,
Lewis JH, Mann RS, Myat AM;
WPI; 96-425379/42.
N-PSDB; T40092.
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| Aabel= ElR
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| 208..238
| Alabel= ELR1
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                                                                                                                                                                                                                                                                                                                                                                                   C-Serrate; Notch; cell differentiation; cell fate; tissue repair; central nervous system; cancer; therapy; diagnosis.
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/note- "region of homology with Drosophila Delta
and Serrate, predicted to mediate binding
with Notch"
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truncation of the encoding cDNA clone"
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/label= Extracellular_domain
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Chick Serrate.
C-Serrate; Notch; cell differentiation;
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/label= Sig_peptide
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W05835 standard; Protein; 1193 AA.
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/label- ELR4
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'label= ELR2
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'label- ELR3
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'label= ELR7
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Chicken Serrate (WDS83), or C-Serrate, is a ligand for the zygotic neurogenic locus Notch and is believed to play a major role in determining cell fates in the central nervous system. Its amino acid sequence was deduced from a cDNA clone (T40092) obtid. from an optic explant cDNA library. C-Serrate is expressed in the central nervous system, cranial placodes, nephric mesoderm, vascular sequence 1193 AA; 234 qycdkciphpgcvhgtciepwqclcetnwggqlcdkdlnycgthppclnggtcsntgpdk 375 VLTCSDKPC-HQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNCSPNPCINGGSC dinecasnpcmngghcqdeingfqclcpagfsgnlcqldidycepnpcqngaqcfnlamd qvasasgqfeleilsvqnvngvlqngnccdgtrnpgdkkctrdecdtyfkvclkeyqsrv 174 crprddffthhtcdqngnktclegwtgpecnkaicrqgcspkhgsctvpgecrcqygwqg 349 iddcspnpcghggtcqd----l-v--dgfkcicppqwtgktcqldanecegkpcvnansc ä Indels 28; Ish-Horowicz Length 1193;

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cell fate; centra
diagnosis; antibo
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central nervous
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491..528
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Human Serrate-1 (W05833) and human Serrate-2 (W05833) are ligands for the zygotic neurogenic locus Notch, and are believed to play a major role in determining cell fates (differentiation) in the central nervous system. Their amino acid sequences were deduced from CDNA clones (see also T40090-91) isolated from human foetal brain cDNA libraries. The proteins, antibodies raised to them, and encoding nucleic acids can be used in the detection of serrate sequences and in the treatment of disorders of cell fate
                                                          serrate-1; blood cell;
                                                                       Proliferation and differentiation Proliferation; differentiation; su
                                                                                                                          W18354;
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sytllveaw-dssnd-tvqpdsi-iekashsgminpsrqwqtlkqntgvahfeyqirvtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lllallc-alrakvcgasgqfeleilsmqnvngelqngnccggarnpgdrkctrdecdty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96-425379/42.
                                                                                                                                                                                                  HNGGTCMNRVNSFECVCANGFRGKQC
                                                                                                                                                                                                                                                                                                                                                                                      ANGWSGKMCEEKVLTCSDKPC-HQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDN
                                                                                                                                                                                                                                                                                                                                                                                                                    spgwtgptcstniddcspnncshggtcqd----l-vng--fkcvcppqwtgktcqldane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCE---HGHCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLTAFICFTVIVQVH-SSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCL-GSCKTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRPCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRVCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWPG
                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T40090.
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.4%;
llarity 41.9%;
Conservative
              Location/Qualifiers
                                                                                                                                     protein;
                                                          neuron;
                                                                                                                                       1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score Pred.
                                                          ion suppression polypeptide.
; suppression; human; delta-1;
leukaemia; malignant tumour;
                                                                                                                                       B
                                                                                                                                                                                                                                560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e 1692; DB 19;
. No. 7.98e-132;
Mismatches 193;
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474

421 415 362 362 302 307 242 247 184

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Query Match
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Matches
                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                    fkvclkeyqsrvtaggpcsfgsgstpviggntfnlkas-rgndr---nrivlpfsfawpr 130
                                                                                                                                                                                                                                                                                                                             sytllveaw-dssnd-tvqpdsi-iekashsgminpsrqwqtlkqntgvahfeyqirvtc 187
:::|:||||| |::|
                                                                                                                                                                                                                                                                                                                                                                    247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spgwtgptcstniddcspnncshggtcqd----l-vng--fkcvcppqwtgktcqldang 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANGWSGKMCEEKVLTCSDKPC-HQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSPNPCINGGSCQP-SGK--CICPAGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQ 478
                                                                                                                                                                                                                                                                                         16 lllallc-alrakvcgasgqfeleilsmqnvngelqngnccggarnpgdrkctrdecdty 74
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                                                                                                                   - suppress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nggtcsntgpdkyqcscpegysgpnceiaehaclsd--pchnrgsc-ke--tslgfecec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ceakpcvnakscknliasyycdclpgwmgqncdinindclg-qcqndascrdlvngyrci
                                                                                                                                              Claim 15; Page 83-91; 114pp; Japanese.

The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement oblood formation, e.g. after immunosuppression.
                                                                                                                                                                                                                                       Length 1218;
                                                                                                      N-PSDB; 170175.
Peptide(s) encoded by human genes delta-1 and serrate-1 - su
proliferation and differentiation of undifferentiated human
/label- Signal
32..1218 .
/label- Differentiation_suppression_protein
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                          108; Mismatches 194;
                                                                                                                                                                                                                                       Score 1680; DB 25;
Pred. No. 8.74e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qngaqcynrasdyfckcpedyegknc 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 12
W18351 standard; protein; 1036
                                                                              KK.
                                                                                                                                                                                                                                       / Match 27.3%;
Local Similarity 41.5%;
                                                         30-NOV-1995; JP-311811.
17-NOV-1995; JP-299611.
(ASAH ) ASAHI KASEI KOGYO
                                                                                                                                                                                                                                                          235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                       29-MAY-1997.
15-NOV-1996; J03356.
                                                                                       Itoh A, Sakano S;
WPI; 97-298110/27.
                            WO9719172-A1
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                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W18351;
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                    75
                                                                                                                                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
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ID W1
AC W1
DT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 ciphpgcvhgicnepwqclcetnwggqlcdkdlnycgthqpclnggtcsntgpdkyqcsc 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement of blood formation, e.g. after immunosuppression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress proliferation and differentiation of undifferentiated human blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             csfgsgstpviggntfnlkas-rgndr---nrivlpfsfawprsytllveaw-dssnd-t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 syyodclpgwmgqncdinindclg-qcqndascrdlvngyrcicppgyagdhcerdidec
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Proliferation and differentiation suppression polypeptide. Proliferation; differentiation; suppression; human; delta-1; serrate-1; blood cell; neuron; leukaemia; malignant tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1676; DB 25;
Pred. No. 1.94e-130;
104; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells
Claim 5; Page 66-71; 114pp; Japanese.
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W18352 standard; protein; 1187 AA.
W18352;
                                                                                                                                                                                                                                                                                                                        29-MAY-1997.
15-WOY-1995; J03356.
30-NOV-1995; JP-311811.
17-NOV-1995; JP-299611.
(ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 27.28;
Similarity 42.18;
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                                                                                                                                                                       immunosuppression.
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WPI; 97-298110/27
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WO9719172-A1.
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RESULT 14
ID W05834
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ASAH) ASAHI KASEI KOGYO KK.
Itoh A. Sakano S;
WPI: 97-298110/27.
Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress proliferation and differentiation of undifferentiated human blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-1997.
15-NOV-1996; J03356.
30-NOV-1995; JP-311811.
17-NOV-1995; JP-299611.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serrate-1; blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppression.
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 standard;
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231; Conservative
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and differentiation suppression polypeptide.
n; differentiation; suppression; human; delta-1
lood cell; neuron; leukaemia; malignant tumour;
Protein; 1257
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Pred.
104; M
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No. 1.
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human; delta-1;
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 12-SEP-1996. U03172. 
07-MAR-1995; US-400159. 
07-MAR-1995; US-400159. 
(IMCR ) IMPERIAL CANCER R 
(UYYA ) UNIV YALE.
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Artavanis-Tsakonas
Lewis JH, Mann RS,
WPI; 96-425379/42.
                                                                            WO9627610-A1.
                                                                                                                   domain
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28-JAN-1997
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934..125
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719..735
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tissue repair; th
                   Ish-Horowicz
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Two Drosophila ganomic phage libraries were screened and recombinant clones were isolated. The CDNAs in lambda gat10 were isolated from an early pupal library. The Cl CDNA was isolated from an early pupal library. Subsequently the C3 CDNA was isolated using the 5' 700 bp terminal fragment of the C1 CDNA as probe. The complete 5561bp
                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                Gaps
          Vertebring Sorrate protein and related DNA - used to treat or prevent malignancies characterised by increased Notch activity. Claim 5; Page 104-107; 161pp; English.

Human Serrate-1 (W0583) and human Serrate-2 (W05833) are ligands for the zygotic neurogenic locus Notch, and are believed to play a major role in determining cell fates (differentiation) in the central nervous system. Their amino acid sequences were deduced from CDNA clones (see also T40090-91) isolated from human foetal and encoding nucleic acids can be used in the detection of Serrate sequences and in the treatment of disorders of cell fate
                                                                                                                                                                                                                                                                                                                                                                                                              224 DYCHIPKCAKGCE--HGHCDKPNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 GWGGLYCNQDLNYCTNHRPCKNGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNP
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Pred. No. 6.38e-102;
73; Mismatches 138; Indels 19;
                                                                                                                                                                                                                                                          Length 1257;
                                                                                                                                                                                             or differentiation, partic. cancer, nervous system disorders and in tissue repair or regeneration.
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the study and manipulation of differentiation and other
physiological processes
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Serrate; toporythmic protein; family.
Drosophila melanogaster.
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WPI; 93-214095/26.
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R38304 standard; Protein; 1404
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Best Local Similarity 43.5%;
Matches 177; Conservative
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11-DEC-1991; U09240.
11-DEC-1991; WO-U09240.
(UYYA.) UNIV YALE.
                                                                                                                                                                                                                              1257 AA;
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Gaps 35;
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                                                                                                                                                                                                                                                                                                                       CLLTAFICFTVIVQ-VHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLG-S-CK 62
sequence of DNA of the Drosophila Serrate protein was derived from C1 and C3 cDNAs (Q43910). The deduced protein product appears to be a transmembrane protein. AAs 51-80 represent the likely signal peptide; ass 542-564 represent potential membrane associated region; ass 1221-1245 represent the putative transmembrane domain. Sequence 1404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aphsagiaanalltttataiigsnlsstallaaltsavastslaigpcinakecrnqpgs
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                                                                                                                                                                                                                           Indels 46;
                                                                                                                                                                         Score 1258; DB 7; Length 1404;
Pred. No. 2.42e-94;
143; Mismatches 199; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: Fri Jun 12 11:50:28 1998
                                                                                                                                                                      vuery match 20.4%;
Best Local Similarity 34.8%;
Matches 207; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 12 11:58:33 1998; MasPar time 6.47 Seconds 737.017 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-083-590A-2 (1-833) from US08083590A.pep (1 of 2) 6164 1 MHWIKCLLTAFICFTVIVQV......GSGAGTAQQQRSVVCGTPHM 833

Searched: 62624 seqs, 5720858 residues Scoring table:

PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 34.579; Variance 176.081; scale 0.196

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 13 14 16 17 18 19 20 20 22 23 23 | 1111 120 1211 1211 1211 1211 1211 1211 | Result No. |
|---|--|---------------------|
| 388 379 287 292 277 238 238 238 238 238 238 238 238 238 | 6164 1514 660 660 654 654 647 512 493 470 452 | Score |
| | 100.0 24.6 10.7 10.7 10.6 10.6 10.5 8.3 8.3 8.3 8.3 | % Query Match |
| 1833 1394 2409 1257 673 673 673 675 | 833 203 383 385 385 1480 1293 2199 1810 1910 | Length I |
| ω ω μ μ μ μ μ ω μ ω χ | 2122121111 | B |
| PCT-US95-0 5177197-30 US-08-264- 5180808-2 US-08-340- US-08-264- US-08-435- US-08-435- US-08-435- 5258288-1 5258288-4 | US-08-264- US-08-264- US-08-457- US-08-597- US-08-597- US-08-597- PCT-US91-0 US-08-264- PCT-US95-1 US-08-264- PCT-US95-1 US-08-264- PCT-US95-1 | ID |
| 0.1, 2, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, | Sequence 6, Applicatio Sequence 3, Applicatio Sequence 2, Applicatio Sequence 2, Applicatio Sequence 1, Applicatio Sequence 1, Applicatio Sequence 2, Applicatio Sequence 9, Applicatio Sequence 4, Applicatio Sequence 4, Applicatio Sequence 3, Applicatio | Description |
| 8.84e 4.53e 6.53e 2.69e 1.11e 3.80e 3.41e 3.41e 3.41e 3.41e 3.19e | 10 0.00e+00 110 1.18e-42 110 1.18e-42 110 3.63e-42 110 3.63e-42 110 1.35e-42 110 1.35e-42 110 1.35e-20 110 3.86e-29 110 2.66e-26 110 7.36e-26 110 8.84e-21 | Pred. No. |

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| US-08-312- | US-08-261- | US-08-170- | 5466668-6 | US-08-587- | US-08-278- | 5256770-7 | US-08-404- | US-08-404- | US-08-404- | US-08-148- | US-08-448- | US-08-435- | US-08-435- | US-08-282- | us-07-907- | US-08-436- | US-07-985- | US-08-267- | US-08-282- | US-08-435- | US-08-435- |
| Sequence 1, Applicatio | Sequence 59, Appl | Sequence 54, Appl | Patent No. 5466668 | Sequence 1, Applicatio | Sequence 25, Applicati | | | Sequence 4, Appli | Sequence 4, Appli | Sequence 12, Appl | Sequence 12, Appl | Sequence 3, Appli | Sequence 3, Appli | Sequence 4, Appli | Sequence 1, Appli | • | • | • | ` | • | Sequence 2, Appli |
| catio | Applicati | Applicati | 8 | catio | icati | Õ. | Applicatio | Applicatio | Applicatio | Applicati | Applicati | Applicatio | Applicatio | Applicatio | icatio | Applicatio | Applicatio | icatio | Applicatio | Applicatio | catio |
| 5.30e-05 | 5.30e-05 | 5.30e-05 | 5.30e-05 | 8.69e-05 | | 1.96e-05 | 6.09e-06 | 6.09e-06 | 6.09e-06 | 5.76e-07 | 5.76e-07 | 1.25e-07 | 1.25e-07 | | 1.25e-07 | 1.25e-07 | 1.25e-07 | 1.25e-07 | . 32e | 5.32e-08 | 5.32e-08 |

ALIGNMENTS

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|--|--|--|---------|---|----|--------|--------------------------------|-------------------------------------|----|--|---|--------|--|--------------------------------------|-------------|--------|--|
| TELEPHONE: 212 790-9990 TELEPHONE: 212 790-9990 TELEPAX: 212 8698864/9741 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 833 amino acids TYPE: amino acid | ATTORNEY AGENT INFORMATION: NAME: Mistrock, S. Leslie REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 7326-004 TRIFCOMMINICATION INFORMATION: | CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/695,189 FILING DATE: 03-MAY-1991 | 264,534 | IBM PC compatible SYSTEM: PC-DOS/MS-DOS | | \sim | CITY: New York STATE: New York | STREET: 1155 Avenue of the Americas | SS | INVENTION: In Toporythmic Proteins, And Me SEQUENCES: 34 | APPLICANT: ATTAVANIS-TSAKONAS, SPYRIOON et al. TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains | ON: | Sequence 6, Application US/08264534 Patent No. 5648464 | Sequence 6, Application US/08264534. | 01-JAN-1900 | XXXXXX | LT 1 US-08-264-534-6 STANDARD; PRT; 833 AA. |

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APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 564464ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWPGTFSLIVEAWHDTNNSGNAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 YGDVITPILGENSVNLTDAQRFQNKGFINPIQFPFSFSWPGTFSLIVEAWHDTNNSGNAR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTCDLNYYGSGCAKFCRPRDDS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 GSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFRVCLKHYQATIDITSQCT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 THKLLIQRLLVQQVLEVSSEWKTHKSESQYTSLEYDFRVTCDLNYYGSGCAKFCRPRDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1514; DB 1; Length 203;
Pred. No. 2.06e-113;
0; Mismatches 0; Indels
                                                                                                                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 AA
                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                          us 07/695,189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
ENCE 203 AA; 22840 MW; 218129 CN;
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                                                                                                                                                                                                                                                                                                                                                                                           ATTOKNEL PORENT.

NAME: MASTOCK, S. LESIIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 8698864/9741
TELEFAX: 512 8698864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acids
           Sequence 3, Application US/08264534
Patent No. 5648464
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08457135
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 FGHSTCSETGEIICLTGWQGDYC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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unknown
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Best Local Similarity 100.0%;
Matches 203; Conservative
                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: U.S.A.
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ID US-08-457-135-2
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                                                                                                                                                                                                                                                                                                                                                                                                                  PGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGPCHN 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 PGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGPCHN 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 SLGGKTGSNSGLTFDGGNPNIIKNTWDKSVNNICASAAAAAAAAAADECLMYGGYVASV 720
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                                                                                                                                                                                    121 SWPGTFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDF 180
                                                                                                                                                                                                                                                                                      181 RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCEHGHC 240
                                                                                                                                                                                                                                                                                                                                           241 DKPNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRP 300
                                                                                                                                                                                                                                                                                                                                                                                                    CKNGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCSPNPCINGGSCQPSGKCICPAGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQCV 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTCMNRVNSFECVCANGFRGKQCDEESYDSVTFDAHQYGATTQARADGLTNAQVVLIAV 600
                                                                                                                             Gaps
                                                                                                                1 MHWIKCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGS
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                                                                                                                                                                       61 CKTRFRVCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSF
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                                                         Length 833;
                                                                                     0; Indels
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                                                      Score 6164; DB 1;
Pred. No. 0.00e+00;
0; Mismatches 0
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           MOLECULE TYPE: protein
TENCE 833 AA; 88812 MW; 3155492 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08264534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                      Match
Local Similarity 100.0%;
es 833; Conservative
    unknown
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US-08-264-534-3
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                                                                                           US-08-597-545-2
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
Sequence 2,
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                               33 QNGFCEDDNVCRCQPGWQGPLCDQCVTSPGCLHGLCGEPGQCICTDGWDGELCDRDVRAC
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEGLSTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/304/NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
STRAIN: Human
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APPLICATION NUMBER: 07/9
FILING DATE: 11-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LABORDA, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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                                                                                                                                      NCDLQLDNCSPNPCINGGSC-QPS--G-KCICPAGFSGTRC
                                                                                                                                                           TCSRPVTNCASSPCQNGGTCLQHTQVSYECLCKPEFTGLTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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89; Conser
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383 AA; 41201 MW; 758273 CN;
                      Application US/08597545
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larity 40.3%;
Conservative
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Application US/08597545
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Delta-Like Gene Expressed
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Pred. No. 1.18e-42;
Pred. No. 1.18e-67;
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                                                      01-JAN-1900
                                Sequence 1, Application US/08597545
                                                                             XXXXXX
                                                                                                   US-08-597-545-1
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Sequence 1, Application Patent No. 5580738
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                                                                                                                                                                                                                                                 93 SSA-PCANNGTCVSLDDGLYECSCAPGYSGKDCQKKDGPCVINGSPCQHGGTCVDD-EGR
                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
STRAIN: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0: FILING DATE: 11-DEC-1992 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300 TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                        TGY-KCHCANGWSGKMCEEKVLTCSDKPC-HQGICRNVRPGLGSKGQGYQCECPIGYSGP
                                                                                                                                               NCDLQLDNCSPNPCINGGSC-QPS--G-KCICPAGFSGTRC 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3000 K St. CITY: Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Similarity 40.3%;
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383 AA; 41201 MW; 758273 CN;
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                                                                                                   STANDARD;
           US/08597545
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Pred. No. 1.18e-42;
50; Mismatches 67
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NUMBER OF SEQUENCES:
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ORIGINAL SOURCE:
STRAIN: Mouse
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Pred. No. 3.63e-42;
50; Mismatches 82; Indels 13; Gaps 10;
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Delta-Like Gene Expressed In
                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,545
                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 007/989,537
FILING DATE: 11-DEC-1992
ATTORNEY,AGENT INFORMATION:
NAME: BENT Stephen A.
RESISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELECHONE: (202)672-5300
TELECAX: (202)672-5300
TELECAX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 AA
                              Neuroendocrine Tumors
                                                      Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                       IN: Mouse Dlk
385 AA; 41320 MW; 772804 CN;
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                                                                                        ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: 1:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                       CITY: Washington, D.C. COUNTRY: USA
                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                Match 10.6%;
Local Similarity 37.0%;
les 85; Conservative
GENERAL INFORMATION:
APPLICANT: LABORDA,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                  FILING DATE:
                                                        ADDRESSEE:
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US-08-457-135-1
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Sequence 2, Application PC/TUS9109055
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon
TITLE OF INVENTION: Purified SLIT protein and Sequence Elements Thereof
NUMBER OF SEQUENCES: 9
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Pred. No. 3.63e-42;
50; Mismatches 82; Indels 13;
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ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,135
FILING DATE: 10-1095
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/989,537
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
NAME: BENT, Stephen A.
NAME: CONTRACT OF THE CONTR
APPLICANT: LABORDA, Jorge
IIILE OF INVENTION: Delta-Like Gene Expressed
IIILE OF INVENTION: Neuroendocrine Tumors
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
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385 AA; 41320 MW; 772804 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9109055.
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Matches 85; Conservative
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  428
                          956
                                                             898 GRVRNDILAKC-N-ACFEQPCQNQAQCVALPQREYQCLCQPGYHGKHCEFMIDACYGNPC 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1480 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 972-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                GKMCEEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNCSPNPC
                                                                                                                                                                                        IDENTIFICATION METHOD: experimental oTHER INFORMATION: developmentally regulated
                                                                                                                                                                                                                                                               OTHER INFORMATION: prot NAME/KEY: 7th EGF-like LOCATION: 1353 to 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212
TELEX: 236268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Barth, Richard J. REGISTRATION NUMBER: 28,180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/
FILING DATE: 7-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PFILING DATE: 19911127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 246 Church Street STREET: Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Yale University
ADDRESSEE: Office of Cooperative Research
                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                       IDENTIFICATION METHOD: OTHER INFORMATION: In
                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: signal sequence LOCATION: 1 to 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 06510
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                                                                                                                                         rification METHOD: experimental
1480 AA; 165751 MW; 10400770 CN
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                                                                                               Conservative
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                                                                                                                                                                  COOH-terminal region 1405 to 1480
                                                                                                                                                                                                                  Alternative splice segment 1394 to 1404
                                                                                                                                                                                                                                                                                                             Tandem EGF-like repeats 911 to 1150
                                                                                                                                                                                                                                                                                                                                                           Four Flank-LRR-Flank domains 37 to 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linear
                                                                                                         10.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                       OD: similarity to epidermal growth 
Involvement in receptor-ligand
                                                                                                                                                                                                                                                                                                                                    mediates adhesive events
                                                                                                                                                                                                                                                                                      protein-protein interactions
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                                                                                                                                                                                                                                                                          ke repeat
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                                                                                             Score 647; DB 2;
Pred. No. 1.35e-41;
56; Mismatches 66
                                                                                                                                                                                                                                                                                                   similarity to tandem EGF-like
                                                                                                                                                                                                                                                                                                                                                                                              similarity to other signal
                                                                                                                                                                                                                                                                                                                                               Array of Flank-LRR-Flank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.50 inch. 800 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              900964/RSB
                                                                                              Mismatches 66;
                                                                                                                                            CN;
                                                                                                                     Length 1480;
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175 FRWTKSFTLILQA-LDMYNTSYPDAERLIEETSYSGVILP-SPEWKTLDHIGRNARITYR 232
                                                122 TAFRLCLKEYQTTEQGASISTGCSFGNATTKILGGSSFVLSDP------G-VGAIVLPFT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08264534 Patent No. 5648464
                        63
                                                                                                  63 CNLIALI-LILLVHKISAAGNFELEILEISNTNSHLLNGYCCGMPAELRATKTIGCSPCT 121
                                                                                                                         y Match 8.3%;
Local Similarity 35.8%;
hes 86; Conservative
                                                                                                                                                                                                                                        TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                          6 CLLTAFICFTVIVQ-VHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLG-S-CK 62
                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 293 AA; 32286 MW; 438798 CN;
                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 03-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                       TRERVCLKHYQATID-TT-SQ-CTYGDVITPILGENSVNLTDAQREQNKGETNPIQEPES
                                                                                                                                                                                                    TYPE: ami
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
CITY: N
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                              TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                            293 amino acids
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                                                                                                                      Score 512; Db ...
ored. No. 1.15e-30;
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                                                                                                                                                  Length 293;
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                                                                                                                         Gaps
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Sequence 4, Application PC/TUS9511684
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE
TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING SAME
NUMBER OF SEQUENCES: 28
                                                        434 S-QL-RC-PNDCHSRGRC-VEGKCVCEQGFKGYDC-SDMS-C-PNDCHQHGRC---VNG- 482
                                                                                                                                                                           483 MCVCDDGYTGEDCRDR-Q-CP-RDCSNRGLCVD---G-QCVCEDGFTGPDCA-ELS-CPN 533
298 HRPCKNGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTG 357
                                  378 ADCH-NRGRCVDGRCECDDGFTGAD--CGELKCPNGCSGHGRCVNG-QCVCDEGYTGEDC 433
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                                                                                                                                                                                               Score 470; DB 2; Length 1810;
Pred. No. 2.69e-27;
61; Mismatches 145; Indels 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ANDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER, READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10666 North Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                     1810 AA.
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1810 AA; 199304 MW; 17319263 CN;
                                                                                                                                                                                                                                               534 D-CHGQGRC---VNG-QCVCHEGFMGKDCKEQ 560
                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11684
FILING DATE: 14-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,359
FILIND DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application PC/TUS9511684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33,950
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REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: BE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 34.2%;
Matches 135; Conservative
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GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE
TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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                                                                       180 FRVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCEHGH 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 KPNQCVCQLGWKGALCNECV-LEPNCIH-GTCNKPWTCICNEGWGGLYCNQDL--NYCTN 297
120 FSWPGTFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 CDDGFTGEDCSQLACP-SDCNDQGKCVN-GVCICFEGYAAD-CSREICPVPCSEEHGTCV 263
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                                                 233 VRVQCAVTYYNTICTIFCRPRDDQFGHYACGSEGQKLCLNGWQGVNCEEAICKAGCDPVH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Mismatches 154; Indels 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 North Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                         2199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 493; DB 2;
Pred. No. 3.86e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FINCE 2199 AA; 240716 MW; 25336188 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/11684
FILING DATE: 14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,359
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               Sequence 2, Application PC/TUS9511684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/COCKET UNBER: BEC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                       RESULT 9
ID PCT-US95-11684-2
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                                                                                                                                                                                                                            01-JAN-1900
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RESULT 11
ID US-08-254-4
XX
AC XXXXXX
AC XXXXXX
DT 01-JAN-1900
XX Sequence 4, Appli
CC Patent No. 56484
CC FITTLE OF INVI
CC INTEREOF INVI
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   REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Then
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NERAL INFORMATION: APPLICANT: Artava
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                                                                                                    NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
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                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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                                                                                                                                                                                 US 07/695,189
                                                                                                                                                                                                                                                           US/08/264,534
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                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Versi
SOFTWARE: #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ME
TITLE OF INVENTION: CE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                             ATTORNEY/AGENT INFORMATION
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                                                                                                                                          FILING DATE: 3 CLASSIFICATION:
     NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UM
                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 18-FEB-1994
                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US95/02251 FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O. I
                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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Similarity 37.0%;
77; Conservet
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199 AA; 21952 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METHODS AND COMPOSITIONS FOR STIMULATING CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC/TUS9502251
                                                                                                                      US 08/199,780
                                                                                                                                                                               US 08/316,650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 452; DB 1;
Pred. No. 7.36e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   of America
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         UMIC009P--
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                                                                                                                                                                                                                                                                                                                    Version
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BONE

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981 DINECRHPGICPDGRCVNSPGSYTCLACEEGYVGQSGSC-VDVNECLTPGICTHG-RCIN 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1039 MEGSFRCSCEPGYEVTPDKKGCRDVDECASRASCPTGLCLNTEGSFTCSACQSGYWVNED 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  925 YPGYT-LVTLGDTQECQDIDECEQPGVCSGGRCS-NTEG-SYHCECDRGYIMVRKGHCQ- 980
                                                                                                                                                                                                                                                                                                                                                                                                       870 GTCVSLPNG-YRCVCSPGYQLHPSQ-DYCTDDNECMRNPCEGRGRCVN-S-V-GSYSCLC 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, LENA; HELDIN, CARL-HENRIN, TORI, SOLATED NUCLEOTIDE SEQUENCE EXPRESSING HUMAN TRANSFORMING GROWTH FACTOR-BETAI-BINDING PROTEIN NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
RILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                           Score 388; DB 2; Length 1833;
Pred. No. 8.84e-21;
54; Mismatches 104; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1099 GTACEDLDECAFPGVCPTG-VCTNTVGSFSCKDCDQGYR 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.1%; Score 379; DB 3; I Best Local Similarity 31.8%; Pred. No. 4.53e-20;
                                                       APPLICATION NUMBER: US 08/199,780
FILING DATE: 18-FEB-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parker: David L.
REGISTATION NUMBER: 32,165
REFERENCE/POCKET NUMBER: UMIC009P--
TELECOMMUNICATION INFORMATION:
TELEFAX: (713) 789-2679
TELEFX: 79-0924
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1833 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1510 AA; 165567 MW; 12055844 CN;
                                                                                                                                                                                                                                                                                                  :ULE TYPE: protein
1833 AA; 197927 MW; 15940870 CN;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                           Query Match 6.3%;
Best Local Similarity 30.8%;
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5177197.
                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1394
                                                                                                                                                                                                                                                                                  TOPOLOGY:
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5177197-30
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ID 51
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                                                                                                                                                                                                            58; Mismatches 129; Indels 53; Gaps 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING BONE NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          258 NECVLEPN-CIHGICUK-P--WICICNEG-WG-GL--YCNQDLNYCINHRPCKNG-GICF 308
                                                                                                                                                                                                                                                                                                                 309 NTGEGLYTCKCAPGYSGDDCENEIXSCDADVNPCQNGGTCIDEPH-TK-TG-YKCHCANG 365
                                                                                                                                                                                                                                                                                                                                                                             366 WSGKMCEEKVLTCSD-KPCHQ-GICRNVRPGLGSKGQGYQC-ECPIGY-S--GPNCDLQL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                      782 TPGSFQCQCLSGYHLSRDRSRCEDIDECDFPAACI-GGDCINTNGSYRCLCPLGHRLVGG 840
                                                                                                                                                                                                                                       555 DECRLNQNICGHGQCVPGPSDYSCHCNAGYRSHPQHRYCV-DVNECEAE-PCGPGKGICM 612
                                                                                                                                                                                                                                                                                                  613 NTG-GSYNCHCNRGYRLHVGAGGR-SC-VDLNECAKPHLCGDGGFCINFPGHYRCNCYPG 669
                                                                                                                                                                                                                                                                                                                                                            670 YRLK--ASRPPICEDIDECRDPSTCPDGKCE--NKPGSFKCIACQPGYRSQGGGACR-DV 724
                                                                                                                                                                                                                                                                                                                                                                                                                       725 NECSEGTPC-SPGWCEKLPGSYRCTCAQGIRTRTGRLSC-IDVDDCEAGKVCQDG-ICTN 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          841 RKCKKDIDECSQDPGLCLPH-ACENLQGSYVCVCDEGFTLTQ-DQHGCEEVE-QPHH 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        524 KDCSVDIDECSSGP--CHNGGTCMNRVNSFECVCANGFRGKQCDEESYDSVTFDAHQ 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 MVNQYRCQCVPGFH-G-THCSSK-VDLC-LIRPCANGGTCLNLNNDYQCTCRAG--FTG-
                                                                                                                                                                             Length 1251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1833 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/02251 FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                             Score 388; DB 2;
Pred. No. 8.84e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MSTI
                                                                                                                                 MOLECULE TYPE: protein
FENCE 1251 AA; 134551 MW; 7366256 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application PC/TUS9502251
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application PC/TUS9502251.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1251 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                               Query Match 6.3%;
Best Local Similarity 32.8%;
Matches 117; Conservative
                                                                                                        TYPE: amino acid
                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-02251-18
                                                                                                                      TOPOLOGY:
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                                                                                                                                                   SEQUENCE
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Patent No. 5648464

GENERAL INFORMATION:

APPLICANT: Artavanis-Tsakonas, Spyridon et al.

TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               832 CEDINECLEDKSVCQRGD-CINTAGSYDCTCPDGFQ 866
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                       REFERENCE/DOCKET NUMBER: 18.872
REFERENCE/DOCKET NUMBER: 7326-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR CENTER OF THE PENNIE
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 77 amino acids
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rcqcvpgfh--gr--hcsskvdlclirp-canggfclnlnndvqctcragf--rg-kdc 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVDIDEC -- SSGPCHNGGTCMNRVNSFECVCANGFR 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRCTCGQGYQLSAAKDQCED-IDECQHRHLCAHG-QCRNTEGSFQCVCDQGYRASGLGDH 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEPNVCANGDCSNLEGSYMCSCHKGYTRTPDHKHC-RDIDECQQGNLCVNG-QCKNTEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGKMCEEKVLTCSD-KPC-HQGICRNVRPGLGSKGQGYQC-ECPIGYSGPNCD-LQLDNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --RM-TORG-RCEDIDECLNPSTCPDEQC-VNSPG-SYQCVPCTEGFRGWNGQCLDVDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NECVLEPN-CIHGTC-NKP-W-TCICNEG-W-GGLYCN-QDLNYCTN-HRPCKNGGTCFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SPNPCINGGSCQPSG--KCICPAGFSGT---R-CETNIDDCL-GHQCENGGTCIDMVNQ
                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 10036
                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               CITY: New York
                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107;
                                                                                                                                                                                                                                                                                                     New York
Y: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                        Pennie & Edmonds
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                                                                                                                                                     US 07/695,189
                                                                                                                                                                                                      US/08/264,534
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77 amino acids

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Search completed: Fri Jun 12 11:59:15 1998 Job time : 42 secs.
                                                                                                                                                     Matches
                                                                                                                                                                              Query Match
                                                                                                                                                                                                        SEQUENCE
                                                512 DYQCTCRAGFTGKDC
                                                                                                453 NIDDC-LGHQCENGGTCIDMVNQYRCQCVPGFHGTHCSSKVDLCLIRPCANGGTCLNLNN 511
                                                                                                                                                 4.7%;
Local Similarity 40.0%;
ses 30; Conservative
                                                                         62 TERCVCMPGFTGTQC 76
                                                                                                                TYPE: amino acid
STRANDEDNESS: single
STOPOLOGY: unknown
MOLECULE TYPE: peptide
QUENCE 77 AA; 8329 MW; 28
                                                                                                                                                                                                        28450 CN;
                                                                                                                                                   Score 287; DB 1; Lo
Pred. No. 6.52e-13;
17; Mismatches 27;
                                                                                                                                                                            Length 77
                                                                                                                                                    Indels
                                                                                                                                                   <u>بر</u>
                                                                                                                                                   Gaps
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Fri Jun 12 11:50:47 1998; MasPar time 32.48 Seconds 936.820 Million cell updates/sec

1 MHWIKCLLTAFICFTVIVQV......GSGAGTAQQQRSVVCGTPHM 833

Title:
Description:
Perfect Score:
Sequence: >US-08-083-590A-2 (1-833) from US08083590A.pep (1 of 2) 6164

Scoring table: PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries Searched: 120441 segs, 36531193 residues

pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Database:

Statistics: Mean 48.016; Variance 95.108; scale 0.505

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 222118 2322118 2322118 2322118 | Result No. |
|--|----------------|
| 6164 6107 6045 1910 11826 11826 1186 1266 1266 987 957 959 959 953 953 953 953 953 953 953 953 | Score |
| 100.0 99.1 31.0 29.6 22.7 22.7 22.7 12.0 15.7 15.7 14.6 11.1 11.1 11.1 11.1 11.1 11.1 | Query Match |
| 833 832 880 728 1220 1220 1404 1404 1408 1408 2471 1203 1203 1203 2524 2524 2524 2524 2525 2531 2531 2531 2531 2531 2531 2531 | Length |
| <i></i> | DB |
| S19087 S319087 S31246 S300670 I500670 I500670 I48324 A266136 A266136 A24612 A49172 A49172 A49172 A49173 | Ħ |
| gene Delta protein pr neurogenic protein pe gene Delta protein pr C-Delta-1 - chicken DELTA-like 1 - mouse jagged protein precur neurogenic repetitive serrate protein precu gene serrate protein transmembrane protein transmembrane protein transmembrane in mou cell-fate determining fibropellin Ia - sea Xotch protein - Afric notch protein - fruit gene Notch-1 protein notch protein homolog notch protein homolog notch 3 protein - mou fibropellin C precurs Notch homolog Motch p crumbs protein - frui adhesive plaque prote | Description |
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| 388 | 388 | 399 | 447 | 455 | 459 | 460 | 465 | 470 | 495 | 543 | 550 | 616 | 641 | 644 | 647 | 647 | 647 | 654 | 654 | 656 | 660 |
| 6.3 | 6.3 | 6.5 | 7.3 | 7.4 | 7.4 | 7.5 | 7.5 | 7.6 | 8.0 | 8.8 | 8.9 | 10.0 | 10.4 | 10.4 | 10.5 | 10.5 | 10.5 | 10.6 | 10.6 | 10.6 | 10.7 |
| 2907 | 1251 | 2918 | 3566 | 1746 | 293 | 2019 | 647 | 1810 | 2201 | 1295 | 387 | 260 | 1429 | 385 | 1480 | 1469 | 530 | 385 | 383 | 383 | 259 |
| N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N |
| A57278 | A57293 | A54105 | A40701 | S19694 | B26637 | JQ1322 | A43902 | A32230 | A32160 | A32901 | B49175 | A44549 . | S06434 | A54785 | A36665 | B36665 | A31640 | S53718 | S53716 | B45484 | S48713 |
| fibrillin-2 precursor | latent transforming g | fibrillin-2 precursor | tenascin-X precursor | tenascin precursor - | neurogenic repetitive | tenascin precursor - | tenascin - eastern ne | tenascin precursor - | tenascin-C - human | glpl protein precurso | Motch A protein - mou | fetal antigen 1 homeo | homeotic protein lin- | preadipocyte factor 1 | slit protein 1 precur | slit protein 2 precur | epidermal growth fact | homeotic protein dlk | homeotic protein dlk | delta-like dlk homeot | fetal antigen 1 - hum |
| 3.88e-50 | 3.88e-50 | 2.87e-52 | 1.19e-61 | 3.15e-63 | 5.11e-64 | 3.25e-64 | 3.34e-65 | 3.43e-66 | 3.75e-71 | 9.55e-81 | 3.75e-82 | 1.75e-95 | 1.45e-100 | 3.55e-101 | 8.70e-102 | 8.70e-102 | 8.70e-102 | 3.26e-103 | 3.26e-103 | 1.27e-103 | 1.95e-104 |

ALIGNMENTS

| Db 301 CKNGGTCFNTGEGLYTCKCAPGYSGDDCENETYSCDADVNPCQNGGTCIDEPHTKTGYKC | Qy 241 DKPNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRP | Db 241 DKPNQCVCQLGWKGALCNECVLEPNCIHGTCNKFWTCICNEGWGGLYCNQDLNYCTNHRP | OY 181 RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCEHGHC | Db 181 RYTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCEHGHC | QY 121 SWPGTFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDF | Db 121 SWPGTFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYT | OY 61 CKTRFRVCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSF | Db 61 CKTRFRVCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSF | Qy 1 MHWIKCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGS | Db 1 MHWIKCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGS | Query Match 100.0%; Score 6164; DB 2; Length 833; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 833; Conservative 0; Mismatches 0; Indels | <pre>cross-references FlyBase:FBgn0000463</pre> | #gene FlyBase:Dl | GENETICS TOTOTORICES LIBITIONS | ##residues 1-833 ##label MUS | • | ##status preliminary | mind baca mining / cane | Muskavitch, M.A.T. | ACCESSIONS \$19087 | 20-Feb-1995 #sequence_revision 20-Feb-1995 | metanogaster) #formal name Drosophila melanogaster | |
|---|---|---|---|---|---|---|--|--|---|---|---|---|------------------|--------------------------------|------------------------------|---|----------------------|-------------------------|--------------------|--------------------|--|---|-----------------------|
| NGGTCIDEPHTKTGYKC 360 | GGLYCNQDLNYCTNHRP 300 | GGLYCNQDLNYCTNHRP 300 | DYCHIPKCAKGCEHGHC 240 | DYCHIPKCAKGCEHGHC 240 | WKTNKSESQYTSLEYDF 180 | WKTNKSESQYTSLEYDF 180 | REQNKGETNPIQEPESE 120 | REQUEGETNPIQEPESE 120 | RCCSGESDGATGKCLGS 60 | RCCSGESDGATGKCLGS 60 | <pre>Length 833; Indels 0; Gaps 0;</pre> | #checksum 2566 | | | | | | | | | b-1995 #text_change | • | TIME TIME (DIOSOFITIE |

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Muskavitch, M.A.T.
#journal Genes Dev. (1988) 2:1723-1735
#title Complex and encodes a protein related to blood coagulation factors and encodes a protein related to blood coagulation factors and epidermal growth factor of vertebrates.
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#formal_name Drosophila melanogaster
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The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic territories and encodes a putat transmembrane protein with EGF-like repeats.
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                                                                                                                                                                                                    PGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGPCHN
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KEYWORDS transmembrane protein
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                              I50719 #type complete
C-Delta-1 - chicken
#formal_name Gallus gallus #common_name chicken
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
         150719
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denrique,
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                       13-Sep-1996
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#title Transient and restricted expression during mouse embryogenesis of Dll1, a murine gene closely re Drosophila Delta.
#cross-references_MUID:95401858
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#accession IS0719
                    ##black
##molecule_type mRNA
1-722 ##label
         ##cross-references EMBL:X80903;
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##molecule_type mRNA
##residuee
                                                                                                                                                                                                                                                                                                                                                                                                               DLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCSCRPGYTGSSCEIEINECDA--NPCKNGGSCTD-LE-NS-YSCTCPPGFYGKNCELSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPRDDRFGHFTCGERGEKYCNPGWKGQYCTEPICLPGCDEQHGFCDKPGECKCRYGWQGR 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFRVCLKHYQATIDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGP
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Similarity 50.1%;
                                                                                 148324
                                                                                                                                                                        Development
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148324
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DELTA-like 1 - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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Terences EMBL:U26590; NID:g882411; PID:g882412
#length 728 #molecular-weight 79861 #checksum
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Nature (1995) 375:787-790
Expression of a Delta homo
                                                                                                                                                                                                          Bettenhausen, B.;
                                                                                                                                                                                                                                 I48324
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                                                                                                                                                                                           Gossler, A.
                                                            preliminary;
                                                                                                                                                                        (1995) 121:2407-2418
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Pred. No. 0.00e+00;
78; Mismatches 168;
                                                              translated
                                                                                                                                                                                                            de Angelis, M.H.;
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RES
3; NID:g806569;
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                                                                                                                                                                                                                                                                                                           248 WQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNGATCTNTG 307
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                                                                                                                                          Gaps
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#formal_name Rattus norvegicus #common_name Norway rat
28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change
11-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lindsell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, Cell (1995) 80:909-917
Jagged: a mammalian ligand that activates Notchl.
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Y #length 1220 #molecular-weight 134528 #checksum
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Local Similarity 41.4%; Pred. No. 0.00e+00;
les 235; Conservative 110; Mismatches 192; Indels
                                                                                                                                          Indels
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Pred. No. 0.00e+00;
87; Mismatches 166;
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#authors Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ortega, J.A.
#journal EMBO J. (1987) 6:761-766
#title EGF homologous sequences encoded in the genome of Drosophila melanogaster, and their relation to neurogenic genes.
#cross_references_MUID:87218537
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                                                                              124 GTESLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEXDFRVT
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neurogenic repetitive locus delta protein -
(Drosophila melanogaster) (fragment)
#formal_name Drosophila melanogaster
16-Aug-1988 #sequence_revision 16-Aug-1988
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##cross-references GB:X05140; NID:g7851; PID:g929563
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                                                                                                                                                                                                                                                                                                                                        VRVQCAVTYINTTCTTFCRPRDDQFGHYACGSEGQKLCLNGWQGVNCEEAICKAGCDPVH
                                                                                                                                                                                                                                                                                                                                                                                        FSWPGTFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRFRVCLKHYQATID-TT-SQ-CTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAFRLCLKEYQTTEQGASISTGCSFGNATTKILGGSSFVLSDP-----G-VGAIVLPFT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLLTAFICFTVIVQ-VHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLG-S-CK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNLIALI-LILLVHKISAAGNFELEILEISNTNSHLLNGYCCGMPAELRATKTIGCSPCT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTG-YK-CH-CAN-GWSGKMCEE-KVLTC--SDKPCHQGICRNVRPGLGS---KGQ-G--
                                                                                                                                                                                   NHRPCKNGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTC-IDEPH-T
                                                                                                                                                                                                                                                    GHCDKPNQCVCQLGWKGALCNECVLEPNCIHGTCN-KPWTCICNEGWGGLYCNQDLNYCT
                                                                                                                                                                                                                                                                                                                       FRVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCE--H
                                                                                                                                                                                                                                                                                                                                                                                                                   FRWTKSFTLILQA-LDMYNTSYPDAERLIEETSYSGVILP-SPEWKTLDHIGRNARITYR 232
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                                                 YQCECPIGYSGPNCDLQLDNCSPNPCINGGSC-QP-SG-KCICPAGFSGTRCETNIDDCL
                                                                                                                                                   QAQVYRTSHGRSNMGRPVRRSSSMRSLDHLRPEGQALNGSSSSGLVSLGSLQLQQQLAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n 20.5%; Score 1266; DB 2; Length 1404; Similarity 34.8%; Pred. No. 9.53e-231; 207; Conservative 143; Mismatches 199; Indels 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A36666
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serrate protein precursor -
melanogaster)
#forms' --
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19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-Feb-1997
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FEATURE
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REFERENCE
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                                              Matches
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412,452,558,739,
965,977,1004,1030,
1150
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Best Local
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997-1060
1222-1246
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727-796
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288-316
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##residues 1-1351,'T',1353-1408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues
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67 CNLIALI-LILLVHKISAAGNFELEILEISNTNSHLLNGYCCGMPAELRATKTIGCSPCT 125
                                                                            Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHQCEN-GGTCI--DMVNQYR-CQ-CVPGFHGTHCSSKVDLCL-IRPCANGGTCLNLNND
                                              207;
                                                            Similarity
                                                                                                   #binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 1408 #molecular-weight 150645 #checksum 5466
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31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change
16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein; transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Drosophila gene Serrate encodes protein with a complex expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas, U.; Speicher, S.A.; Knust, Development (1991) 111:749-761
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                                              Conservative
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n EGF homology #label EG09\
n EGF homology #status atypical #
n EGF homology #label EG11\
in EGF homology #label EG12\
in EGF homology #label EG13\
in EGF homology #label EG14\
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EGF homology #label EG01\
EGF homology #label EG03\
EGF homology #label EG03\
                                                          Score 1266; DB 2;
Pred. No. 9.53e-231;
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                                              Mismatches
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y #label EG07\
y #label EG08\
#label EG09\
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                                                                        Length 1408;
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                                              Indels 46;
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#label INT\
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Mech. Dev. (1993) 43:87-100
A zebrafish homologue of the Drosophila neurogenic gene Notch
and its pattern of transcription during early
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                                                                                                                                            237 VRVQCAVTYYNTTCTTFCRPRDDQFGHYACGSEGQKLCLNGWQGVNCEEAICKAGCDPVH 296
                                                                                                                                                           GKCDRPGECECRPGWRGPLCNECMYYPGCKHGSCNGSAWKCVCDTNWGGILCDQDLNFCG 356
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                                                                                   FRWTKSFTLILQA-LDMYNTSYPDAERLIEETSYSGVILP-SPEWKTLDHIGRNARITYR 236
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#formal_name Brachydanio rerio #common_name zebra fish
20.reb-1995 #sequence_revision 20-Feb-1995 #text_change
12-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #domain ankyrin repeat homology #label ANI\
#domain ankyrin repeat homology #label AN2\
#domain ankyrin repeat homology #label AN3\
#domain ankyrin repeat homology #label AN5
#length 2437 #molecular-weight 262306 #checksum 4021
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CLLTAFICFTVIVQ-VHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGRCLG-S-CK
                                                                                                                                                                                                                   APHSAGIAANALLITTATAIIGSNLSSTALLAALTSAVASTSLAIGPCINAKECRNQPGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82; Mismatches 124; Indels 34;
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Pred. No. 4
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S42612
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Best Local Similarity 39.1%;
Matches 154; Conservative
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#title
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ORGANISM
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Exp. Cell Res. (1993) 204:364-372

Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety of tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             517
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                                                                                                                                                                                                                362 CANGWSGKMCEEKVLT-CSDKPCHQG-ICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQL 419
                                                                                                                                                                                                                                                                                  928
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                                            301
                                                                                             814
                                                                                                                                         302 KNGGICFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGICIDEPHTKTGYKCH 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence extracted from NCBI backbone (NCBIP:126158)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily unassigned ankyrin repeat proteins; ankyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This protein has many EGF repeats and lin-12/Notch repeats. This protein is one of the neurogenic proteins controlling the decision between ectodermaland neural fate for cells in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Motch B protein - mouse (fragment)
Notch homolog
Notch homolog
11-Jan-1994 #sequence_revision 05-Jan-1996 #text_change
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A49175; PH1570; S32113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 -PWTCICNEGWGGLYCNQDLNYCTNHRPCKNGGTCFNTGEGLYTCKCAPGYSGDDCENEI
                                                                                                                                                                                                                                                                                                                                                                               CVCLAGFRGERCAEDIDECVSAPCRNGGNCTDCVNSYTCSCPAGFSGINCEINTPDCTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGYRCTCKKGFKGYNCQVNIDECASN-PCLNQGTCFDDVSG-YTCHCMLPYTGKNCQTVL
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                          249 QLGWKGALC---NECYLEPNCIHGTC-N--KPWTCICNEGWGGLYCNQDLNYCTNHRPC
                                                                                                                                                                                                                                                                                  869 NECVRNPCTNGGVCENLRGGFQCRCNPGFTGALCENDIDDCEPNPCSNGGVCQDRVNGFV
                                                                                                                                                                                                                                                                                                          PDGFRDATCLSQHNECSSNP-CIHGSCLDQINSYRCVCEAGWMGRNCDININECLSN-PC
                                                                                               VNGGTCKDMTSG-YLCTCRAGFSGPNCQMNINEC-AS-NPCLNQGSCIDD--V-AGFKCN
                                                                                                                                                                                       CMLPYTGEVCEN-VLAPCSPRPCKNGGVCRE-SEDF----QSFSCNCPAGWQGQTCEVDI
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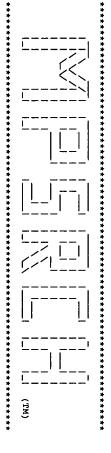
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                                                                                                                                                                                                                                                                                                                CHNTQGSYMCECPPGFSGMDCEEDINDCLANPCQNGGSCVDKVNTFSCLCLPGFVGDKCQ 947
                                                                                                                                                                                                                                                                                                                                                                                                                      YTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCHCANGWSGKMCEEK 374
                                                                                                                                           SFECVCANGFRGKQC
                                                                                                                                                                                                               SKYDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSYDIDECSSGPCHNGGTCMNRYN
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Similarity 44.1%;
#40136 #type complete
fibropellin Ia - sea urchin (Strongylocentrotus
epidermal growth factor homolog precursor
alternatively spliced fibropellin Ib (EGFI)
#formal_name Strongylocentrotus purpuratus #comm
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#domain ankyrin repeat homology #label AN2:
#domain ankyrin repeat homology #label AN3:
#domain ankyrin repeat homology #label AN3:
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#length 2471 #molecular-weight 265367 #checks
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Development (1992) 116:931-941
Notch2: a second mammalian Notch
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cell-fate determining gene Notch2 protein - rat
#formal_name Rattus norvegicus #common_name Norway rat
21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
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#journal Science (1987) 237:1487-1490
#title A sea urchin gene encodes a polypeptide
epidermal growth factor.
#cross-references MUID:87319677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hunt, L.T.; Barker, W.C.
FASEB J. (1989) 3:1760-1764
Avidin-like domain in an epidermal growth
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13-May-1992 #sequence_revision 17-Sep-1997 #text_change
20-Mar-1998
A40136; B40136; C40136; A29316; A43131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #superfamily Clr/Cls repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Mol. Evol. (1989) 29:314-327
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                                                                               in C11/C1s repeat homology #label CSR\
in EGF homology #label EGF2\
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EGF homology avidin-like
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#label
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#title Xotch, the Xenopus homolog of Drosophila notch.
#cross-references WIID:90385285
#accession A35844
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##residues 1-2703 ##label KID
                                                                                                  1-2524 ##label COF
                                                                                                                                            transmembrane protein
                                                        preliminary;
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A24420; A24768
A24420
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Local Similarity 36.0%;
nes 134; Conservative
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##molecule_type mRNA
                                                                                    ##molecule_type mRNA
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                                                                                                   ##residues
                                                                                                                 CLASSIFICATION
                                                           ##status
                                                                                                                                                                                                                                                             Query Match
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1991-2023
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Matches
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Xotch protein - African clawed frog
#formal_name Xenopus laevis #common_name African clawed frog
12-oct-1990 #sequence_revision 12-oct-1990 #text_change
12-sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 DKPCHQG-ICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNCSPNPCINGGSC-QP-S 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 CLNGGICVDGV-NM-FECTCLAGFTGVRCEVNIDECASA-PCQNGGICIDGING-YTCSC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 PLGFSGDNCENNDDECSS-I-PCLNGGTCVD--LVNA-YMCVCAPGWTGPTCADNIDECA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 SAPCQNGGVC--I-DGV--NG--YMCDCQPGYTGTHCETDIDECARPPCQNGGDCVDGVN 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               #disulfide_bonds #status predicted
#length 1064 #molecular-weight 112072 #checksum 303
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                                                                                                                                                                                                    #disulfide_bonds #status predicted\
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Coffman, C.; Harris, W.; Kintner, C.
Science (1990) 249:1438-1441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 556 ANGFRGKOCDEESYDSVTF 574
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Best Local Similarity 40.4%;
Matches 129; Conservative
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848-857,864-875,
869-884,886-895,
902-913,907-922,
924-933
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641-656, 658-667,
674-685, 679-694,
696-705, 712-723,
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772-781,788-799,
793-808,810-819,
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522-533,527-542,
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#authors
#journal
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1-48,'I',50-118,'R',120-230,'I',232-256,'N',258-266,'A',
268-872,'R',874-958,'R',960-1970,'FH',1973-2256,'G',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 LGSKGQGYQCECPIGYSGPNCDLQLDNCS--PNPCINGGSCQPS-G--KCICPAGFSGTR 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 CNPSPCLNGGTCRQTD-DISYDCTCLPGFSGQNCEENIDDCPSNNCRNGGTCVDGVNTYN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 CQCPPDWTGQYCTEDVDECQLMPNACQNGGTCHNTYGG-YNCVCVNGWTGEDCSENIDDC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               449 CEIDVNECLSNPCQNDSTCLDQIGEFQCICMPGYEGLYCETNIDECASNPCLHNGKCIDK 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509 INEFRCDCPTGFSGNLCQHDFDECTSTPCKNGAKCLDGPNSYTCQCTEGFTGRHCEQDIN 568
                                                                                                                         *superfamily unassigned ankyrin repeat proteins; ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A24420 #type complete inotch protein - fruit fly (Drosophila melanogaster) #formal_name Drosophila melanogaster 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change
                                                                                                                                                                                                                                                                                                                                                                         9441
      not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 CICNEGWGGLYCNQDLNYCT-NHRPCKNGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 -ANA-ACHSGATC-HD-RVASFY-CECPHGRTGLLCHLDN-ACISNPCNEGSNC-DTNP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNGKA--I-CTCPPGYTGPACNNDVDECSLGANPCERGGRCTNTLGSFQCNCPQGYAGPR
eliminary; nucleic acid sequence not shown; compared with conceptual translation
                                                                                                                                                                                                                                            #domain ankyrin repeat homology #label ANI\
#domain ankyrin repeat homology #label ANZ\
#domain ankyrin repeat homology #label AN3\
#domain ankyrin repeat homology #label ANS\
#domain ankyrin repeat homology #label ANS\
#length 2524 #molecular-weight 274931 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 953; DB 2; Length 2524;
Pred. No. 5.56e-165;
95; Mismatches 113; Indels 30;
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#gene notch
##cross-references FlyBase:FBgn0004647
#introns 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
CLASSIFICATION #superfamily notch protein; ankyrin repeat homology; EGF
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FEATURE
1950-1982
1983-2015
2017-2049
2050-2082
2083-2115
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Search completed: Fri Jun 12 11:53:23 1998 Job time : 156 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.4%;
Best Local Similarity 39.1%;
Matches 148; Conservative
                                                                                              571 SVTFDAHQYGATTQARADG
                                                                                                                                          833 CVT-NPCGNGGTCIDKVNG 850
                                                                                                                                                                                      773 NEFICHCPPGYTGKRCELDIDECSSNPCQHGGTCYDKLNAFSCQCMPGYTGQKCETNIDD 832
-|::| | :|:|| | :|:|| | | :|:|| | | | :: |
511 NDYQCTCRAGFTGKDCSYDIDECSSGPCHNGGTCMNRVNSFECVCANGFRGKQCDEESYD 570
                                                                                                                                                                                                                                                                                       451
                                                                                                                                                                                                                                                                                                             713 EKNVDECISSPCANNGVCIDQVNGYKCECPRGFYDAHCLSDVDECASNPCVNEGRCEDGI 772
                                                                                                                                                                                                                                                                                                                                                                               394 GLGSKGQGYQCECPIGYSGPNCDLQLDNCSPNPCINGGSC-QP-SG-KCICPAGFSGTRC 450
                                                                                                                                                                                                                                                                                                                                                                                                       658 - VGS----YYCQCQAGTSGKNCEVNVNECHSNPCNNGATCIDGINSYKCQCVPGFTGQHC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 CDADVNPCQNGGTCIDEPHTKTGYKCHCANGWSGKMCEEKVLTCSDKPCH-QGICRNVRP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606 CDS--NPCHRG-KCIDD--VNS-FKCLCDPGYTGYICQKQINECESNPCQFDGHCQD-R- 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             548 FKCSCALGETGARCQINIDDCQSQ-PCRNRGICHDSIAG-YSCECPPGYIGTSCEININD 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 WTCICNEGWGGLYCNQDLNYCTNHRPCKNGGTCFNTGEGLYTCKCAPGYSGDDCENEIYS 334
                                                                                                                                                                                                                                                                                     ETNIDDCLGHQCENGGTCIDMVNQYRCQCVPGFHGTHCSSKVDLCLIRPCANGGTCLNLN 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain ankyrin repeat homology #label AN1\
#domain ankyrin repeat homology #label AN2\
#domain ankyrin repeat homology #label AN3\
#domain ankyrin repeat homology #label AN4\
#domain ankyrin repeat homology #label AN5
#domain ankyrin repeat homology #label AN5
#domain ankyrin repeat homology #label AN5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the authors translated the codon ATC for residue 49 as Thr. ATT for residue 2044 as Arg, GTA for residue 2265 as Ala, CGC for residue 2407 as His, and CTT for residue 2445 as Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##label WHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2258-2264,'V',2266-2406,'R',2408-2444,'L',2446-2703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 951; DB 2; Length 2703; Pred. No. 1.45e-164; 83; Mismatches 116; Indels 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6404
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 12 11:53:42 1998; MasPar time 21.43 Seconds 974.872 Million cell updates/sec

Tabular output not generated.

Title: >US-08-083-590A-2
Description: (1-833) from US08083590A.pep (1 of 2)
Perfect Score: 6164

Sequence: 1 MHWIKCLLTAFICFTVIVQV......GSGAGTAQQQRSVVCGTPHM 833
Scoring table: PAM 150
Gap 11

Searched: 69111 seqs, 25083644 residues
Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 50.001; Variance 79.902; scale 0.626

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 3 5 5 5 5 7 6 7 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 | V | Result No. |
|--|------------------------|----------------|
| 1819 1986 1986 1989 1959 1959 1959 1959 1959 1959 1959 | 6045 1826 | Score |
| 77888455664936 | 98.1 29.6 | Query Match |
| 714 1408 2437 1064 2793 2793 2793 2531 2531 2434 2318 2318 2318 2318 2318 2318 2318 2318 | 880 722 | Length |
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ALIGNMENTS

| DR DR | | 2 2 2 | | 88 | 888 | ឧឧ | នន | នន | នន | R. | ₽ ? | R | Z Z | Ŗ, | ₽ ₹ | RP | R R | RA ? | R | 88 | GN GN | DE DI | DŢ | i i | 38 | RESULT |
|---|--|-----------|------------------------|----------|------------------------|--|--|---|--|---------|---|---------------------------|-----|------------|---|-------------------------------|----------------------------|--|-----|---|----------|---|-----------|-------|---------------------------------|--------|
| PS00022; EGF_1; 9. PS01186; EGF_2; 9. PS01187; EGF_CA; 2. | HSSP; P00/25; ICBH. FLYBASE; FBgn0000463; Dl. PROSITE: PS00010: ASX HYDROXYL: 3. | A26637; 1 | ; X06289; ; X05140; | IMILARIT | FOR BINDING WITH THE N | THIS PROCESS IS UNDER CONTROL OF THE NEUROGENIC GENES!- NOTCH AND SERRATE MAY INTERACT AT THE PROTEIN LEVEL, IT IS | -!- SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO THE INNER PART OF EMBRYO IS ONE OF THE FIRST STEPS OF CNS DEVELOPMENT IN INSECTS, | CELL LINEAGES i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. | -i- FUNCTION: ESSENTIAL FOR PROPER DIFFERENTIATION OF ECTODERM. DL IS REQUIRED FOR THE CORRECT SEPARATION OF NEURAL AND EPIDERMAL | (1990). | MEDILINE; 91209240. HAENLIN M., KRAMATSCHEK B., CAMPOS-ORTEGA J.A.; | PATTERN OF TRANSCRIPTION. | [3] | TEGA J.A.; | KNUST E., DIETRICH U., TEPASS U., BREMER K.A., WEIGEL D., VAESSIN H., | SEQUENCE OF 422-621 FROM N.A. | EMBO J. 6:3431-3440(1987). | VAESSIN H., BREMER K.A., KNUST E., CAMPOS-ORTEGA J.A.; | [1] | UKOSOPHILA MELANOGASIEK (EKOIT ELI). EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA. | DL. | O1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) NEUROGENIC LOCUS DELTA PROTEIN PRECURSOR. | (REL. 10, | (REL. | DL_DROME STANDARD; PRT; 880 AA. | LT 1 |

540

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SMGGKTGSNSGLTFDGGNPNIIKNTWDKSVNNICASAAAAAAAAAAAAADECLMYGGYVASV -720
                                                                                    ADNNNANSDFCVAPLQRAKSQKQLNTDPTLMHRGSPAGTSAKGASGGGPGAAEGKRISVL
                                                      HCRNGWSGKMCEEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLD
                                                                                                                   PGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGPCHN
                                                                                                                                                 GGTCMNRVNSFECVCANGFRGKQCDEESYDSVTFDAHQYGATTQARADGLANAQVVLIAV
                                                                                                                                                                                FSVAMPLVAVIAACVVFCMKRKRKRAQEKDNAEARKQNEQNAVATMHNGSAVGVALASA
                       CKNGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKC
                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                             781 GEGSYCSQRWPSLAAAGVAGDLFIQLMAAASVAGTD-GTAQQQRSVVCGTPH 831
                                                                                                                                                                                                                                                                                     DLL1_MOUSE STANDARD; PRT; 722 AA. 061483; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) DELTA-LIKE PROTEIN 1 PRECURSOR (DELTA1).
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                                                                                                    , CALCIUM-BINDING (POTENTIAL).
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                                                                                                                    CALCIUM-BINDING (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 880;
                                            CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 7, CALCIUM-BINDIN
EGF-LIKE 9, CALCIUM-BINDIN
                            EXTRACELLULAR (POTENTIAL) POTENTIAL.
NEUROGENESIS; REPEAT; TRANSMEMBRANE;
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5 -> A (IN REF. 2).
5 -> T (IN REF. 2).
E967E662 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 6045; DB 1;
Pred. No. 0.00e+00;
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llarity 98.0%;
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                                                                                                                                                                                                                                                               TVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFRVCLKHYQA
                 EEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNCSPNPCINGG
                                                                            EGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTC
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llarity 48.0%;
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Pred. No. 0.(
87; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.

DELTA-LIKE PROTEIN 1.

EXTRACELULAR (POTENTIAL)

CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 3.

EGF-LIKE 5.

EGF-LIKE 5.

EGF-LIKE 6.

EGF-LIKE 7.

EGF-LIKE 8.

BY SIMILARITY.

BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM-BINDING
                                                                             IDEPHTKTGYKCHCANGWSGKMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING
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P97677;
01-NOV-1997
01-NOV-1997
01-NOV-1997
DELTA-LIKE P
DISULFID
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TRANSMEM
DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL;
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DISIBIO G., HEBSHI L., BOULTER J., WEINMASTER G.;

SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- FUNCTION: MAY BE INVOLVED IN CELL-TO-CELL COMMUNICATION IN

MAMMALIAN EMBRYOS. MAY HAVE A ROLE IN CELLULAR INTERACTIONS

UNDERLYING SOMITOGENESIS AND DEVELOPMENT OF THE NERVOUS SYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATTUS NORVEGICUS (I
EUKARYOTA; METAZOA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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- SIMILARITY: (
- SIMILARITY: (
BL; U78889; G1
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 G1699046;
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. 35, LAST SEQUI
. 35, LAST ANNO!
IN 1 PRECURSOR
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EGF_1; 8.
EGF_2; 8.
EGF_CA; 2.
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 CHORDATA;
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LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDAT
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POTENTIAL
CYTOPLASMIC
CYTOPLASMIC
CYTOPLASMIC
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 8.
EGF-LIKE 7.
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EGF-LIKE 8.
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EXTRACELLULAR
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Y SIMILARITY
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IKE DOMAINS.
LTA PROTEIN.
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C THIS PROCESS IS UNDER CONTROL OF THE NEUROGENIC GENES.
THIS PROCESS IS UNDER CONTROL OF THE NEUROGENIC GENES.
C CONCEIVABLE THAT THE SERRATE AND DELTA PROTEIN LEVEL, IT IS
CONCEIVABLE THAT THE SERRATE AND DELTA PROTEINS MAY COMPETE
FOR BINDING WITH THE NOTCH PROTEIN.
C -!- SIMILARITY: TO THE DROSOPHILA NEUROGENIC LOCUS DELTA PROTEIN.
EMBL; X56811; G8564; -.
EMBL; X3666; A36666.
PIR; S16878; S16878.
R PIR; S16878; S16879.
R PIR; S16878; S16879.
R PROSITE; PS00010; ASX_HYDROXYL; 7.
R PROSITE; PS01187; EGF_1; 14.
R PROSITE; PS01187; EGF_2; 8.
R PROSITE; PS01187; EGF_2; 8.
R PROSITE; PS01187; EGF_2; 5.
                                                                                                                                                                                                                                                                                                                                                        EGF-LIKE 1.

EGF-LIKE 1.

EGF-LIKE 1.

EGF-LIKE 4.

EGF-LIKE 4.

EGF-LIKE 4.

EGF-LIKE 5.

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EGF-LIKE 7.

EGF-LIKE 9.

EGF-LIKE 9.

EGF-LIKE 9.

EGF-LIKE 10.

EGF-LIKE 10.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 12.

EGF-LIKE 13.

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EGF-LIKE 13.

EGF-LIKE 14.

EGF-LIKE 13.

EGF-LIKE 13.

EGF-LIKE 14.

EGF-LIKE 14.

EGF-LIKE 15.

EGF-LIKE 17.

EGF-LIKE 17.

EGF-LIKE 18.

EGF-LIKE 19.

                                                                                                                                                                                                                                                                                     POTENTIAL.
SERRATE PROTEIN.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                     1408
1223
1249
1408
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4406
477
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5506
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597
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SIGNAL 1
CHAIN 84
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      17;
                                                                                                                                                                                                                                                                                     307
                                                                                                                                                                                                                                                                                                                                                              QGSYTCSCRPGYTGANCELEVDEC-AP-SPCRNGGSCTD-LED-S-YSCTCPPGFYGKVC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                    371
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                                                                                                                                                                                 TDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDEHYYGEGC 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 9109966.

MEDLINE; 9109966.

PLEMING R.J., SCOTTGALE T.N., DIEDERICH R.J., ARTAVANIS-TSAKONAS S.; GENES DEV. 4:2188-2201(1990).

- FUNCTION: ESSENTIAL FOR PROPER ECTODERMAL DEVELOPMENT. SERRATE MAY REPRESENT AN ELEMENT IN A NETWORK OF INTERACTING MOLECULES OPERATING AT THE CELL SURFACE DURING THE DIFFERENTIATION OF CERTAIN TISSUES.

- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

- TISSUE SPECIFICITY: APPEARS TO BE RESTRICTED EXCLUSIVELY TO CELLS OF ECTODERMAL ORGIN.

- TELSOUR SPECIFICITY: APPEARS TO BE RESTRICTED EXCLUSIVELY TO CELLS OF ECTODERMAL ORGIN.
                                                                                                                                                                     SVSPEPPCTYGSAVTAVLGVDSFSLPDGAGI-DPAFSNPIRFPFGFTWPGTFSLIIEALH 127
                                                                                                           68
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO THE INNER PART
                                                                                                           14 ALLCOVWSSGVFELKLQEFVNKKGLLGNRNCCRGGS-GPP--C--ACRTFFRVCLKHYQA
                                                                                                                                                                                                                                                                                                                                                                                                                                    EGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCHCANGWSGKMC
                                                                                                                                                                                                                                                                                                                                                WQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNGATCTNTG
                                                                              Indels 22;
                                               Length 714;
                                                                              82; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DROSOPHILA MELANOGASTER (FRUIT FLY).
EURARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGANC 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1819; DB 1;
Pred. No. 0.00e+00;
      POTENTIAL.
604B76D1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERR_DROME STANDARD; PRT; 1408 AA. 181869.
01-NOY-1990 (REL. 16, CREATED)
01-UL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-FEL-1996 (REL. 33, LAST ANNOTATION UPDATE)
SER OR BD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 91347903.
THOMAS U., SPEICHER S.A., KNUST E.;
DEVELOPMENT 111:749-761(1991).
    476 P
77378 MW;
                                                29.5%;
48.8%;
                                                              Local Similarity 48.8%;
les 253; Conservative
                   714 AA;
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      CARBOHYD
SEQUENCE
                                                Query Match
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                                                                              Matches
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01-NOV-1995
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; | CCECPIGYSGPNCDLQLDNCSPNPCINGGSC-QP-SG-KCICPAGFSGTRCETNIDDCL
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143; Mismatches 199;
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    A BIERKAMP C., CAMPOS-ORTEGA J.A.;

A BIERKAMP C., CAMPOS-ORTEGA J.A.;

L MECH. DEV. 43:87-100(1993).

C MECH. DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF THE EMBRYO DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF THE NURLAR LOCATION: TYPE I MEMBRANE PROTEIN.

C:-- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C:-- DEVELOPMENTAL STAGE: EXPRESSED IN ALL CELLS IN PREGASTRULATION STAGES. DURING GASTRULATION IS DIFFERENTIALLY EXPRESSED, ACCUMULATING FREDOMINATILY IN THE PREGISORAL MESODERM AND ACCUMULATING PREDOMINATILY IN THE PREGISORAL MESODERM AND ACCUMULATING ANIS INCLUDING THE DEVELOPING NEURAL PLATE AND DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING AND DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING MESODERM. ALSO PRESENT IN THE DEVELOPING
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-!- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PRI-
-!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 6 ANK REPEATS.
-!- SIMILARITY: CONTAINS 6 ANK REPEATS.
EMBL; X69088; G433867; -.

PROSITE: PS00010; ASX, HYDROXYL; 23.
PROSITE: PS00010; ASX, HYDROXYL; 23.
PROSITE: PS01186; EGF-2; 28.
PROSITE: PS01187; EGF-CA; 22.
DIFFERENTIATION; NEUROGENESIS; REPEAT; ANK REPEATS.
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VERTEBRATA; PISCES; GNATHOSTOMATA;
CYPRINIFORMES.
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SCIENCE 237:
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FFBP1_STRPU
P10079;
01-MAR-1989
01-FEB-1996
01-FCB-1996
01-NOV-1997
FIBROPELLIN
(UEGF-1).
                                                  AND ZYGOTICALLY.

ALTERNATIVE PRODUCTS: TWO FORMS (IB) LA

-!- SIMILARITY: CONTAINS 21 EGF-LIKE DOMAINS.

-!- SIMILARITY: CONTAINS 1 CUB DOMAIN OF THIS PF
TO AVUIDIN/STREPTAVIDIN.

EMBL; L08692; G161466; --

EMBL; L08692; G161466; --

EMBL; L08692; G161466; --

EMBL; X17530; G667061; --

EMBL; X17533; G667062; --

EMBL; X1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHÂRACTERIZATION.
MEDLINE; 91265254.
BISGROVE B.W., ANDREWS M.E., RAFF R.A.;
DEV. BIOL. 146:89-99(1991).
-!-- FUNCTION: FORM THE APICAL LAMINA, A COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVIDIN-LIKE DOMAIN.
MEDLINE; 89196806.
HUNT L.T., BARKER W.C.;
FASEB J. 3:1760-1764(1989).
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MEDILNE; 90112459.
DELGADILLO-REYNOSO M.G., ROLLO
J.MOL. EVOL. 29:314-327(1989).
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                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: EXTRACELLULAR. IN VESICLES IN THE CYTOPLASM OF UNFERTILIZED EGGS, THEN TO THE BASE OF THE HYALIN LAYER THROUGHOUT DEVELOPMENT AND FINALLY IN THE APICAL LAMINA IN LATE EMBRYOS AND EARLY LARVAE.

DEVELOPMENTAL STAGE: MODERATE LEVELS IN UNFERTILIZED EGGS AND DURING EARLY CLEAVAGE, THEN RAPIDLY INCREASES IN ABUNDANCE BETWEEN LATE MORULA AND MESENCHYME BLASTULA STAGES TO MAXIMAL LEVELS MAINTAINED THROUGH SUBSEQUENT STAGES. EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVCLAGFRGERCAEDIDECVSAPCRNGGNCTDCVNSYTCSCPAGFSGINCEINTPDCTES
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E; 87319677.
D.A., ANDREWS M.E., RAF
E 237:1487-1490(1987).
  PS00010; ASX_HYDROXYL;
PS00022; EGF_1; 19.
'PS00577; AVIDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REL. 10, CREATED)
(REL. 33, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANOMATION UPDATE)
I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED
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; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;
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LACKS
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8 EGF REPEATS.
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    PROSITE; PS01
PROSITE; PS01
PROSITE; PS01
BIOTIN; ALTER
GLYCOPROTEIN.
  DOMAIN
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; PS01186; EGF_2; 19.
; PS01187; EGF_CA; 19.
ALTERNATIVE SPLICING;
  \begin{array}{c} 8.78 \\ 8.28 \\ 8.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.22 \\ 2.
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EGF-LIKE 10, CA
EGF-LIKE 11, CA
EGF-LIKE 12, C
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KINTNER C.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY EMBRYOS.
-!- SIMILARITY: CONTAINS 36 GGF-LIKE DOMAINS.
-!- SIMILARITY: THIS PROTEIN INCLUDES 3 COPIES OF A LIN/NOTCH REPEAT.
-!- SIMILARITY: THIS PROTEIN INCLUDES 3 COPIES OF A LIN/NOTCH REPEAT.
-!- SIMILARITY: CONTAINS 6 ANK REPEATS.
-!- SIMILARITY: THIS PROTEIN INCLUDES 3 COPIES OF A LIN/NOTCH REPEAT.
-!- SIMILARITY: THIS PROTEIN 1 KEPEATS.
-!- SIMILARITY: THIS PROTEIN 1 KEPEAT; BGF-LIKE DOMAIN;
-!- SIMILARITY: GLASSEN 1 KENNEMBRANE: SIGNAL, GLYCOPROTEIN.
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31, CALCIUM-BINDING (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                       NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 5.

EGF-LIKE 5.

EGF-LIKE 6.

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EGF-LIKE 9.

EGF-LIKE 10.

EGF-LIKE 10.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 12.

EGF-LIKE 13.

CALCIUM-BINDING (POUR 11.)

EGF-LIKE 14.

EGF-LIKE 14.

EGF-LIKE 15.

CALCIUM-BINDING (POUR 11.)

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EGF-LIKE 17.

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Pred. No. 3.37e-205;
71; Mismatches 99; Indels 20
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COFFMAN C., HARRIS W., KINTNER C.;
SCIENCE 249:1438-1441(1990).
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REVISIONS TO 1759-1782.
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EGF-LIKE 11, CALCIUM-BINDING (POTEWTIAL).
EGF-LIKE 12, CALCIUM-BINDING (POTEWTIAL).
EGF-LIKE 13, CALCIUM-BINDING (POTEWTIAL).
EGF-LIKE 14, CALCIUM-BINDING (POTEWTIAL).
EGF-LIKE 16, CALCIUM-BINDING (POTEWTIAL).
EGF-LIKE 17, CALCIUM-BINDING (POTEWTIAL).
EGF-LIKE 20, CALCIUM-BINDING (POTEWTIAL).
EGF-LIKE 21, CALCIUM-BINDING (POTEWTIAL).
EGF-LIKE 21, CALCIUM-BINDING (POTEWTIAL).
EGF-LIKE 22, CALCIUM-BINDING (POTEWTIAL).
EGF-LIKE 23, CALCIUM-BINDING (POTEWTIAL).
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C. 1- SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN.
C. 1- SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN.
C. 1- SIMILARIY: SONE OF THE FIRST STEPS OF CNS DEVELOPMENT IN INSECTS,
THIS PROCESS IS UNDER CONTROL OF THE NURSCENCE.
C. 1- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
C. 1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
C. 1- SIMILARITY: THIS PROTEIN INCLUDES 3 COPIES OF A LIN/NOTCH REPEAT.
C. 1- SIMILARITY: CONTAINS 6 ANK REPEATS.
C. 1- SIMILARITY: THIS POSSON.
C. 1- SIMILARITY: THIS PROPERTY.
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CURR. BIOL. 1:120-122(1991).
-!- FUNCTION: NOTCH PROTEIN IS ESSENTIAL FOR PROPER DIFFERENTIATION OF
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8, CALCIUM-BINDING (POTENTIAL).
9, CALCIUM-BINDING (POTENTIAL).
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FINENCE: FENDANCE; INTE.
PROSITE; PS00010; ASX_HYDROXYL; 22.
PROSITE; PS01186; EGF_2; 28.
PROSITE; PS01187; EGF_CA; 22.
PROSITE; PS01187; EGF_CA; 22.
PROSITE; PS01187; EGF_CA; 22.
PROSITE; PS01187; EGF_CA; 22.
TRANSMEMBRANE; SIGNAL; GLYCOPROTEIN.
                                                                                                                                                                                                                                              MEDLINE; 85099329.
WHARTON K.A., YEDVOBNICK B., FINNERTY V.G., ARTAVANIS-TSAKONAS S.;
CELL 40:55-62(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.

BURGGENIC LOCUS NOTCH PROTEIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
36 X EGF-TYPE REPEATS.
EGF-LIKE 1.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
CALCIUM-BINDING (POTE EGF-LIKE 5.
EGF-LIKE 7.
CALCIUM-BINDING (POTE EGF-LIKE 9.
                                                                    WHARTON K.A., JOHANSEN K.M., XU T., ARTAVANIS-TSAKONAS S.;
CELL 43:567-581(1985).
        EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-8 FROM N.A.
MEDLINE; 87-27846.
RELLEY M., ILL., YOUNG M.W.;
MOL. CELL. BIOL. 7:1545-1548(1987).
                                                                                                                                          STRAIN-OREGON-R;
MEDLINE; 87064624.
KELLEX M.R., YOUNG M.W.;
MOLD S.J. BIOL. 6:3094-3108(1986).
                                                                                                                                                                                                                            SEQUENCE OF 2505-2611 FROM N.A.
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                                      SEQUENCE FROM N.A. MEDLINE; 86079539.
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                  HIPKC-AKGCEH
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1. No. 3.91e-2
Mismatches 1
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3.91e-203;
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RESULT TO COLUMN MESSAGE TO CO
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REARCO DEL AMO F., SMITH D...

A GREENSPAN R.J., MCMAHON A.P., GRIDLE: ...

A GREENSPAN R.J., MCMAHON A.P., GRIDLE: ...

L DEVELOPMENT 115.737-744(1992).

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SUBCELLULAR TYPAGE: EXPRESSED ALMOST UNIFORMLY IN COLOR TYPE IN THE PROTEIN IN COLOR TYPE IN THE PROTEIN IN COLOR TYPE PROTEIN IN COLOR TYPE PROTEINS.

CC -!- SIMILARITY: CONTAINS 6 ANK REPEATS.

CC -!- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.

CC -!- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.

CR EMBL, Z11886; G288503; -.

DR EMBL; Z11886; G288503; -.

ASX_HYDROXYL; 22.
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MEDLINE; 93194170.

FRANCO DEL AMO F., GENDRON-:

COPELAND N.G., GRIDLEY T.;

GENOMICS 15:259-264(1993).
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Q01705;
Q1.NOV-1995 (REL.
Q1-FEB-1996 (REL.
Q1-FEB-1996 (REL.
NEUROGENIC LOCUS NOTCH1 OR MOTCH.
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MEDLINE; 93048835.
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EUKARYOTA; METAZOA; CHORDATA;
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; EGF_2; 27.
; EGF_CA; 21.
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EARLY

EMBRYOS

N.A.,

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EGF-LIKE 2.

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EGF-LIKE 6.

EGF-LIKE 1.

EGF-LIKE 7.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10.

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C -: SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
C -: SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
C -: SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
C -: SIMILARITY: CONTAINS 6 ANK REPEATS.
EMBL; XS7405, 637635; -.
R PROSITE: PS00010; ASX, HYDROXYL; 22.
R PROSITE: PS01187; EGF-1; 35.
R PROSITE: PS01187; EGF-2; 26.
R PROSITE: PS01187; EGF-2; 26.
R PROSITE: PS01187; EGF-2; 21.
R PROSITE: PS01187; EGF-2; EGF-2; EGF-2; EGF-2; EGF-2; EGF-2; EGF-2; EGF-2; EGF
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RA MEDLINE: 92111383.

RA MEDLINE: 92111383.

RA WEINMASTER G., ROBERTS V.J., LEMKE G.;

RA MEDLINE: 92111388.

R. DEVELOPHENT 113:199-205(1991).

C. -1 FUNCTION: REQUIRED FOR THE CORRECT DIFFERENTIATION OF A NUMBER OF TISSUES.

C. -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. -1 SUBCELLULAR LOCATION: TYPE IN THE EMBRYO, HIGHEST LEVELS OCCUR BETWEEN CC.

-1 DAYS 12 AND 14 AND DECREASE RAPIDLY TO MUCH LOWER LEVELS IN THE NOTE: AND 14 AND DECREASE RAPIDLY TO MUCH LOWER LEVELS IN THE NOTE: AND 14 AND DECREASE RAPIDLY TO MUCH LOWER LEVELS IN THE NOTE: AND 14 AND DECREASE RAPIDLY TO MUCH LOWER LEVELS IN THE NOTE: AND 14 AND DECREASE RAPIDLY TO MUCH LOWER LEVELS IN THE NOTE: AND 14 AND 14 AND 15 AND 
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                                                                                                                                                465 ATCLDQIGEFQCICMPGYEGVYCEINTDECASSPCLHNGHCMDKIHEFQCQCPKGFNGHL 524
                  Score 928; DB 1; Length 2531;
Pred. No. 3.32e-197;
82; Mismatches 113; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        KDGVATFTCLCQPGYTGHHCETNINECHSQ--PCRHGGTC-QD-RDNS-YLCLCLKGTTG
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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                     Query Match
Best Local Similarity 38.7%;
Matches 147; Conservative
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PREDLINE; 91347367.

X MEDLINE; 91347367.

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X ELLISEN L.W., BIRD J., WEST D.C., SORENG A.L., REYNO SMITH S.D., SKLAR J.;

C CELL 66:649-661(1991).

-i- FUNCTION: MAY BE IMPORTANT FOR NORMAL LYMPHOCYTE OF THE PROPERTY OF TRANSFORMATION CONTRIBUTE TO TRANSFO
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
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NTC1_HUMAN STAN
P46531;
01-NOV-1995 (REL. 3
01-NOV-1995 (REL. 3
01-FEB-1996 (REL. 3
NEUROGENIC LOCUS NO
ASSOCIATED NOTCH PF
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.. 32, LAST SEQUENCE UPDATE)
.. 33, LAST ANNOTATION UPDATE)
.. NOTCH PROTEIN HOMOLOG 1 PRECURSOR
L PROTEIN TAN-1) (FRAGMENT).
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Best Local S
Matches 12
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NTC3_MOUSE
Q61982;
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NOTCH3.
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MEDLINE; 95001556.
LARDELLI M., DALSTRAND J., LE
MECH. DEV. 46:123-136(1994).
                                                                                                                  EUTHERIA;
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EUKARYOTA; METAZOA;
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                                                                                                                  RODENTIA
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7 (REL. 35, LAST SEQUENCE UI
7 (REL. 35, LAST ANNOTATION
LOCUS NOTCH 3 PROTEIN.
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                       LENDAHL
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Pred. No. 1.43e-192;
86; Mismatches 113;
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                       u.;
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       MGD; MGI:99460; NOTCH3.
PROSITE; PSO0010; ASX_HYI
PROSITE; PSO00022; EGF_1;
PROSITE; PSO1186; EGF_2;
PROSITE; PSO1187; EGF_CA
DIFFERENTIATION; NEUROGGE
   TRANSMEM
DOMAIN

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DEVELOPMENTAL STAGE: CNS DEVELOPMENT.
SIMILARITY: CONTAINS 34 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 5 CDC10/SW16 REPEATS.
SIMILARITY: CONTAINS 6 CDC10/SW16 REPEATS.
                                                                                                                                    ; ASX_HYDROXYL;
; EGF_1; 33.
; EGF_2; 27.
; EGF_CA; 17.
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5 X CDC10/SW16
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CYTOPLASMIC.
34 X EGF-TYPE RI
3 X LIN/NOTCH RI
6 X CDC10/SW16 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 CHEDAICDINPVSGRAICTCPPGFTGGACDQDVDECSIGANPCEHLGRCVNT-QGSFLCQ 419
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P49013;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FIBROPELLIN C PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 3)
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Pred. No. 1.75e-189;
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BY SIMILARITY.
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555 CANGFRGKQCDEESYDSVT 573
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37.78;
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Matches 143; Conservative
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1723 173
1895 189
2278 227
2318 AA;
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SEQUENCE
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Best Local Similarity
Matches 122; Conse
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BIOTIN; E
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CHAIN
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MEDLINE; 93273088,
BISGROVE B.W., RAFF R.A.;
DEV. BIOL. 157:526-538(1993).
-i- FUNCTION: FORM THE APICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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EUECHINOIDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: EXTRACELLULAR.

DEVELOPMENTAL STAGE: LOW LEVELS IN UNFERTILIZED EGGS AND DURING EARLY CLEAVAGE, THEN RAPIDLY INCREASES IN ABUNDANCE BETWEEN LATE MORULA AND MESENCHYME BLASTULA STAGES TO MAXIMAL LEVELS MAINTAINED THROUGH SUBSEQUENT STAGES.

EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY.

SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 CUB DOMAIN.

SIMILARITY: THE C-TERMINAL DOMAIN OF THIS PROTEIN IS SIMILAR TO AVIDIN/STREPTAVIDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E; PS00022; EGF_1; 8.
E; PS00577; AVIDIN; 1.
E; PS01180; CUB; 1.
E; PS01186; EGF_2; 7.
E; PS01187; EGF_CA; 6.
E; EGF-LIKE DOMAIN; REPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00010; ASX_HYDROXYL;
                                                                                                                14.3%;
larity 43.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
                                                                                                            ECHINODERMATA; ECHINOZOA; ECHINOIDEA;
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                                Score 881; DB 1;
Pred. No. 4.10e-185
61; Mismatches 78
                                                                                                            LAMINA,
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, CALCIUM-BINDING
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                                                                       Length 570;
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                                    18;
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              RESULTANCE REPORT OF THE PROPERTY OF THE PROPE
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MEDLINE; 96281668.

UTTTENDAELE H., MARAZZI G., WU G., YAN Q., SASSOON

UTTTENDAELE H., MARAZZI G., WU G., YAN Q., SASSOON

DEVELOPMENT 122:2251-2259(1996).

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SIMILARITY: CONTAINS 2D EGF-LIKE DOMAINS.

-!- SIMILARITY: CONTAINS 2D EGF-LIKE DOMAINS.

-!- SIMILARITY: CONTAINS 3 LINNOTCH REPEATS.

-!- SIMILARITY: CONTAINS 6 CDC10/SW16 REPEATS.

-!- SIMILARITY: CONTAINS 6 ANK REPEATS.

-!- SIMILARITY: CONTAINS 6 ANK REPEATS.

REMBL; M80456; G1714084; -.

R EMBL; M38072; TYMVT3.

R PIR; A38072; TYMVT3.

R PIR; A38072; TYMVT3.
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P31696; 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

P31697; 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

P31697; 01-NOV-1997 (REL. 26, CHOPATA; VERTEBRATA; TETRAPODA; NUSCULUS (MOUSE).

EUTHERIA; RODENTIA.
                                                     TRANSMEM
DOMAIN
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DOMAIN
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CALLAHAN R.
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ROBBINS J., BLONDEL B.J., GALLAHAN
J. VIROL. 66:2594-2599(1992).
                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                PROSITE; PS00010; ASX HYDROXYL;
PROSITE; PS00022; EGF_1; 28.
PROSITE; PS01186; EGF_2; 21.
PROSITE; PS01187; EGF_CA; 9.
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SEQUENCE FROM N.A.
AND TESTIS;
                                                                                                                                                                             SIGNAL
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MEDLINE; 92194507.
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AGE 1. AGE 2. AG
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EXTRACELLULAR (POT
POTENTIAL.
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EGF-LIKE 1.
EGF-LIKE 3.
EGF-LIKE 4.
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| BY SIMILARITY. | BY SIMILARITY. | BY SIMILARI BY SIM | AAA -> APK MW; 3F16B6 Score 798; Pred. No. 7 73; Mismat |
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| | | | T.S. |
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| EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL). EGF-LIKE 7. EGF-LIKE 7. EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL). EGF-LIKE 10. EGF-LIKE 11. EGF-LIKE 11. EGF-LIKE 11. EGF-LIKE 11. EGF-LIKE 12. EGF-LIKE 13. EGF-LIKE 13. EGF-LIKE 14. EGF-LIKE 14. EGF-LIKE 15. EGF-LIKE 15. EGF-LIKE 15. EGF-LIKE 14. | | EST - LIKE 29. EST - LIKE 27. LIN/NOTCH 1. LIN/NOTCH 3. ANK MOTIF 2. ANK MOTIF 2. ANK MOTIF 2. ANK MOTIF 2. ANK MOTIF 4. ANK MOTIF 6. BY SIMILARITY. | BI SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. |
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XX KNUST E., DIETRICH U., TEPASS U., BREMER K.A.

X VAESSIN H., CAMPOS-ORTEGA J.A.;

EMBO J. 6:761-766(1997).

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-i. FIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
EMBL; M33753; G552087; ALT_SEQ.
EMBL; X05144; E1746; -.

TIR; B36637; B26637.

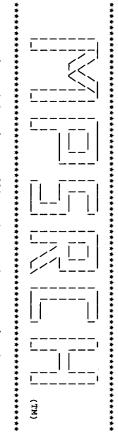
JIR; A35672, B35672.

SSP; P00743; 1APO.

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PROSITE; PS001022; EGF_1; 26.
PROSITE; PS01186; EGF_2; 17.
PROSITE; PS01187; EGF_CA; 15.
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                                                                                          Score 765; DB 1; Length 2139;
Pred. No. 1.93e-155;
96; Mismatches 184; Indels 35;
       REF. 2).
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1955 1955 N -> K (IN REF. 2).
2139 AA; 233619 MW; 2B9D7CB6 CRC32;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 12 11:55:32 1998; MasPar time 38.07 Seconds 921.382 Million cell upda updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-083-590A-2 (1-833) from US08083590A.pep (1 of 2) 6164

MHWIKCLLTAFICFTVIVQV......GSGAGTAQQQRSVVCGTPHM 833

Scoring table: PAM 150 Gap 11

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 48.199; Variance 82.400; scale 0.585

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| \$ 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | Result No. |
|---|----------------|
| 6140 1910 1897 1865 1861 1702 1692 1691 1691 1687 1687 1691 1648 1648 1649 1970 970 970 975 975 | Score |
| 99.6 30.8 30.3 30.3 30.2 27.4 27.4 27.4 27.4 27.4 27.4 27.4 27 | Query Match |
| 832 717 717 723 721 1193 1218 1218 1218 1219 1219 1219 1212 1203 1203 2470 549 2653 406 | Length |
| 3 12 12 2 12 12 12 2 2 2 2 2 2 2 11 2 11 2 11 2 11 2 11 2 11 2 11 2 11 2 11 2 11 11 | DB . |
| Q99108 Q99108 P87357 O00548 Q91902 Q91902 Q9191902 Q15816 O15122 Q9015816 O15722 P78504 P79941 O42347 P79607 Q06008 Q25058 Q25058 Q25058 Q25059 | Ħ |
| NEUROGENIC LOCUS DELTA TRANSMEMBRANE PROTEIN DELTAJ TRANSMEMBRANE P DELTA, X-DELTA-1. C-SERATE-1 PROTEIN (FR TRANSMEMBRANE PROTEIN TRANSMEMBRANE PROTEIN JAGGED PROTEIN JAGGED 1 (TRANSMEMBRAN NOTCH LIGAND X-DELTA-2 C-SERRATE-2 (FRAGMENT) NOTCH PROTEIN HOMOLOG CELL SURFACE PROTEIN FIBROPELLIN IA (FRAGME NOTCH HOMOLOG SCALLOPE FIBROPELLIN III (FRAGM NOTCH HOMOLOG. | Description |
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| 4.4 | - 4 - (| 2 6 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 3 5 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 |
|------------------------|-----------------------|--------------|------------|------------------------|----------------------|--------------------|-----------------------|-----------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-----------|-----------|--------------------|-----------|-----------|---------------------|
| 470 | 201 | 202 | 495 | 508 | 521 | 535 | 550 | 611 | 647 | 650 | 656 | 654 | 674 | 686 | 869 | 727 | 738 | 786 | 798 | 804 | 804 | 805 | 883 | 895 |
| 7.6 | | ۵ ر د | | 8.2 | 8.5 | 8.7 | 8.9 | 9.9 | 10.5 | 10.5 | 10.6 | 10.6 | 10.9 | 11.1 | 11.3 | 11.8 | 12.0 | 12.8 | 12.9 | 13.0 | 13.0 | 13.1 | 14.3 | 14.5 |
| 1810 | 700 | 2002 | 2201 | 403 | 601 | 1095 | 387 | 144 | 530 | 263 | 1722 | 385 | 383 | 473 | 1687 | 1476 | 585 | 1372 | 1964 | 2003 | 955 | 1999 | 752 | 2447 |
| 12 | | J t | S | ω | w | N | 10 | 12 | w | N | w | 10 | 10 | w | 10 | 12 | 10 | ω | 10 | ν | N | Ŋ | 12 | 12 |
| Q90824 | 04323 | 014583 | 015567 | 018375 | Q20204 | Q99458 | 206007 | 012973 | Q24526 | Q99734 | Q19350 | Q62208 | Q62779 | Q25464 | Q61204 | Q90285 | 035675 | P91526 | 035442 | 000306 | Q99466 | Q99940 | 042374 | 013149 |
| CYTOTACTIN 200KD PRECU | NOTCH DECEDED DECEDIN | HEXABRACHION | TENASCIN-C | C901 PROTEIN (FRAGMENT | F40E10.4 (FRAGMENT). | NOTCH4 (FRAGMENT). | NOTCH PROTEIN HOMOLOG | SERRATE-2 (FRAGMENT). | SLIT LOCUS ENCODING A | NOTCH2 TRANSMEMBRANE P | SIMILAR TO EGF-LIKE RE | STROMAL CELL DERIVED P | PREADIPOCYTE FACTOR 1. | ADHESIVE PLAQUE MATRIX | EGF REPEAT TRANSMEMBRA | PUTATIVE EXTRACELLULAR | M-DELTA-LIKE 3 GENE PR | SIMILARITY TO MULTIPLE | NOTCH4. | NOTCH4. | NOTCH4 (FRAGMENT). | NOTCH4. | REC | NOTCH 2 (FRAGMENT). |
| 6.46e-77 | 1 0/0-70 | 3 386-82 | | 1.18e-85 | 1.16e-88 | 6.63e-92 | 2.17e-95 | 1.20e-109 | 4.05e-118 | 7.94e-119 | 3.05e-120 | 9.03e-120 | 1.70e-124 | 2.45e-127 | 3.51e-130 | 4.54e-137 | 1.10e-139 | 3.88e-15 | 5.23e-154 | 1.92e-155 | 1.92e-155 | 1.10e-155 | 2.08e-174 | 2.68e-17 |

ALIGNMENTS

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US-08-083-590A-2-01.rspt

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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
17RANSMEMBRANE PROTEIN C-DELTA-1.
GALLUS GALLUS (CHICKEN).
EUKARYOIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
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                                                          ADNINIANSDFCVAPLQRAKSQKQLINTDPTLMHRGSPAGSSAKGASGGGPGAAEGKRISVL
                                                                      80 EPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPGTFSLIIEALHTDSP
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FSVAMPLVAVIAACVVFCMKRKRKRAQEKDDAEARKONEONAVATMHHNGSGVGVALASA
                   SLGGKTGSNSGLTFDGGNPNIIKNTWDKSVNNICASAAAAAAAAAADECLMYGGYVASV
                              CHITNIS A., LEWIS J., ISH-HOROWICZ
                                                                                                  GEGSYCSQRWPSLAAAGVAGACSSQLMAAASAAGTD-GTAQQQRSVVCGTPHM 832
                                                                                                                                                                                                                                                                                                                                                                                      Indels 16;
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                                                                                                            490 SRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGP 534
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Pred. No. 0.00e+00;
78; Mismatches 168;
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TISSUB-SPINAL CORD;
MEDLINE; 95319507.
HENRIQUE D., ADAM J., MYAT
NATURE 375:787-790(1995).
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50.1%;
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Matches 263; Conservative
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                                                                                                                                                                                                                                                                          Length 832;
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                 EXTRACELLULAR (POTENTIAL).
                                       INTRACELLULAR (POTENTIAL).
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A -> S (IN REF. 2).
5 -> A (IN REF. 2).
5 -> T (IN REF. 2).
CF9ABECI CRC32;
                                                EGF-TYPE REPEATS
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Pred. No. 0.00e+00;
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          DELTA PROTEIN.
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EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 9.
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Best Local :
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SUBMITIED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; Y11760; E307461; -
PROSITE; PS01187; EGF_CA; 2.
SIGNAL; TRANSMEMBRANE; GLYCOPROTEIN; EGF-LIKE D
SIGNAL
1 19
POTENTIAL
20 717
DELTAD TRANSMEMBRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 3

PRELIMINARY; PRT; 71

P87357; PRELIMINARY; PRT; 71

P87357; O1-MAY-1997 (TREMBLREL. 03, CREATED)

O1-MAY-1997 (TREMBLREL. 03, LAST SCOUGN

O1-JAN-1998 (TREMBLREL. 05, LAST ANNOTA

DELTAD TRANSMEMBRANE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DELTAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGYTGKNCTSAVNKCLHNPCHNGATCHEMDNRYVCACIPGYGGRNC
||: | :|: | : | | | | | | | ::| | ::| | ::|
PGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDC
                                                                                                                                                                                                                                                                                     PNPCINGGSC-QPSGK--CICPAGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQCV
                                                                                                                                                                                                                                                                                                                                                                               NQCYCQLGWKGALCNECYLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRPCKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GECKCRVGFSGKYCDDCIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICLKHYQANVSPDPPCTYGGAVTPVLGSNSFQVPES--FPDSSFTNPIPEAFGFTWPGTF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LITAFICETVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFR
                                                                                                                                                                                                                                                                                                                                   SNPCSNDAQCLDLVDSYLCQCPEGFTGTHCEDNIDECATYPCQNGGTCQDGLSDYTCTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EHYYGEGCSVFCRPRDDTFGHFTCGERGEIICNSGWKGQYCTEPICLPGCDEDHGFCDKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 30.8%;
l Similarity 47.7%;
251; Conservative
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717 AA;
  (TREMBLREL.
(TREMBLREL.
(TREMBLREL.
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(TREMBLREL. 03, LAST SEQUENCE UPDATE)
(TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79061 MW;
    04,
05,
CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 0.00e+00;
96; Mismatches 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
DELTAD TRANSMEMBRANE
; 5CC32ECA CRC32;
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VERTEBRATA; PISCES;
CYPRINIFORMES.
                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 157;
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    UPDATE)
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SEQUENCE FROM N.A. MEDLINE; 95319503. CHITNIS A.B., HENF

HENRIQUE

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SEQUENCE FROM N.A.
MEDLINE; 95319507.
HENRIQUE D., ADAM J., MYAT
NATURE 375:787-790(1995).

CHITNIS

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Best Local
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SUBMITTED (JUN-1997) TO EMBL/GEN
EMBL; AF003522; G2197069; -.
PROSITE; PSO1187; EGF_CA; 1.
GLYCOPROTEIN; EGF-LIKE DOMAIN.
SEQUENCE 723 AA; 77956 MW; A
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Q91902;
Q91902;
Q1-NOV-1996
01-NOV-1996
01-JAN-1998
X-DELTA-1.
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HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MANN R.S., GRAY G.E.,
                                                                                                                                                                                     EUKARYOTA;
                                                                                                                                                                                                          XENOPUS
                                                                                                                                                                                                                                                                                                                                                                                                              479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt CSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CANGWSGKMCEEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KNGATCTNTGQGSYTCSCRPGYTGATCELGIDECDP--SPCKNGGSCTD-LE-NS-YSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFSLIVEAWH-DTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261;
                                                                                                                                                                                 LAEVIS (AFRICAN CLAWED TA; METAZOA; CHORDATA; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 30.3%;
Similarity 48.4%;
261; Conservative
                                                                                                                                                                                                                                           (TREMBLREL.)
(TREMBLREL.)
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HENRIQUE
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05,
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                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred.
86; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; TETRAPODA;
                                                                                                                                                                                     VERTEBRATA;
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                                                                                                                                                                                                        FROG)
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No. 0.
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                                                                                                                                                                                                                                                                                                                              721
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0.00e+00;
~es 171;
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                                                                                                                                                                                     TETRAPODA;
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                                                                                                                                                                                                                                               UPDATE)
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GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCINIGGGSYTCSCRPGYTGSNCEIEVNECDA--NPCKNGGSC-SDLE-NS-YTCSCP 357
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                                                                                                                                                                             84; Mismatches 169; Indels 19;.
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PGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDC 526
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MYAT A., HERRIQUE D., ISH-HOROWIC2 D., LEWIS J.;
MYAT A., HERRIQUE D., ISH-HOROWIC2 D., LEWIS J.;
DEV. BIOL. 174:233-24(1996).
EMBL; X9528; E224084; -.
PROSITE; PSOU010; ASX_HYDROXYL; 10.
PROSITE; PSO1187; EGF_CA; 8.
GLYCOPROTEIN; EGF_LIKE DOMAIN.
NON_TER
SEQUENCE 1193 AA; 131039 MW; 55E5FCD1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREWBLREL. 01, CREATED)
01-NOV-1996 (TREWBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREWBLREL. 05, LAST ANNOTATION UPDATE)
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                                                                                                                                  Score 1861; DB 12;
Pred. No. 0.00e+00;
                                                                                       028040EF CRC32;
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NATURE 375:761-766(1995).
EMBL: L42229; G807696; -.
PROSITE; PSO1187; EGE_CA; 2.
GLYCOPROTEIN; EGF-LIKE DOMAIN.
SEQUENCE 721 AA; 79922 MW;
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                                                                                                                                  30.2%;
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Best Local S
Matches 24
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Q90819;
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                                                                            16 LLLALLC-ALRAKVCGASGOFELEILSMONVNGELONGNCCGGARNPGDRKCTRDECDTY 74
             9/
                                                                                                                                                              19 QVHS-SGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCL-GSCKTRFRVCLKHYQATI
                                                                                                                                                                                                                                                                                                          234 QYCDKCIPHPGCVHGTCIEPWQCLCETNWGGQLCDKDLNYCGTHPPCLNGGTCSNTGPDK
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                                                                                                                                                                                                                                                                                                                                                                                          294 YQCSCPEGYSGQNCEIAEHACLSD--PCHNGGSCL-E--TSTGFECVCAPGWAGPTCTDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 IDDCSPNPCGHGGTCQD----L-V--DGFKCICPPQWTGKTCQLDANECEGKPCVNANSC
                                                                                                                                                                                                                         174 CRPRDDFFTHHTCDQNGNKTCLEGWTGPECNKAICRQGCSPKHGSCTVPGECRCQYGWQG
                                                        61 TAGGPCSFGSKSTPVIGGNTFNLKYS-R--NNE-KNRIVIPFSFAWPRSYTLLVEAW-DY
                                                                                                                                           NDNS-TNPDRI-IEKASHSGMINPSRQWQTLKHNTGAAHFEYQIRVTCAEHYYGFGCNKF
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SEQUENCE FROM N.A.
GRAY G.E., MANN R.S., MITSIADIS E., HENRIQUE D., CARACANGIU M.,
ISH-HOROWICED., ARTHVANIS-TSAKONAS S.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, 01276, 14138937, -
PROSITE; PSO1187; EGF.CA; FRANSMEMBRANE; GLYCOPROTEIN; EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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BDLINE; 95211842.
LINDSEL. C.E., SHAWBER C.J., BOULTER J., WEINMASTER
CELL 80:909-917(1995).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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1218 AA; 133739 MW; E8D64FED CRC32;
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01-NOV-1996 (TREMBLREL. 01, L
01-JAN-1998 (TREMBLREL. 05, L
TRANSMEMBRANE PROTEIN JAGGED
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551 FECVCANGFRGKQC 564
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EUTHERIA; PRIMATES.
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                                                                                                                                           Query Match
Best Local S
Matches 23
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O14902;
O1-JAN-1998
O1-JAN-1998
O1-JAN-1998
                                                                                                                                                                                                                              SEQUENCE FROM N.A.

BASH J., ZONG W.-X., GELINAS C.;

BASH J., ZONG W.-X., GELINAS C.;

SUEMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; AP028593; G2599082; -.

PROSITE; PS01187; EGF_CA; 8.

TRANSMEMBRANE; GLYCOPROTEIN; EGF-LIKE DOMAIN.

SEQUENCE 1218 AA; 133798 MW; 07B97EE3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 95211842.
LINDSELL C.E., SHAWBER C.
CELL 80:909-917(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TRANSMEMBRANE PROTEIN JAGGED 1.
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                                                                         LLLALLC-ALRAKVCGASGQFELEILSMQNVNGELQNGNCCGGARNPGDRKCTRDECDTY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPPGYAGDHCERDIDECASNPCLNGGHCQNEINRFQCLCPTGFSGNLCQLDIDYCEPNPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONGAQCYNRASDYFCKCPEDYEGKNC 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSPNPCINGGSCQP-SGK--CICPAGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEAKPCVNAKSCKNLIASYYCDCLPGWMGQNCDININDCLG-QCQNDASCRDLVNGYRCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGGTCSNTGPDKYQCSCPEGYSGPNCEIAEHACLSD--PCHNRGSC-KE--TSLGFECEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRPCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEXDFRVTC
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FKVCLKEYQSRVTAGGPCSFGSGSTPVIGGNTFNLKAS-RGNDR----NRIVLPFSFAWPR 130
                                             LLTAFICFTVIVQVH-SSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCL-GSCKTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HNGGTCMNRVNSFECVCANGFRGKQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGDCRCQYGWQGLYCDKCIPHPGCVHGICNEPWQCLCETNWGGQLCDKDLNYCGTHQPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDYYYGFGCNKFCRPRDDFFGHYACDQNGNKTCMEGWMGPECNRAICRQGCSPKHGSCKL
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                                                                                                                                                236;
                                                                                                                                                                  Similarity 41.78;
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                109;
                                                                                                                                                                       Score 1691; DB 2; Pred. No. 0.00e+00;
                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOULTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATA;
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                                                                                                                                                Mismatches 192;
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                                                                                                                                                                                           Length 1218;
                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G.;
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S B

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FRVCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWPG

124

FKVCLKEYQSRVTAGGPCSFGSGSTPVIGGNTFNLKAS-RGNDR---NRIVLPFSFAWPR 130

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                                              Query Match
Best Local S
Matches 23
                                                                                         SEQUENCE FROM N.A.

ODA T., ELKAHLOUN A.G., MELTZER
GENOMICS 43:375-379(1997).

EMBL; AF003837; G2228793; .

EMBL; PROSITE; PS01187; EGF_CA; B.

GLYCOPROTEIN; EGF-LIKE DOMAIN.
SEQUENCE 1218 AA; 133858 MW;
                                                                                                                                                                                                                                                                                                          015122
015122;
01-JAN-1998
01-JAN-1998
01-JAN-1998
                                                                                                                                                                                            SEQUENCE FROM N.A.

ODA T., ELKAHLOUN A.G., PIKE
PICCOLI D.A., MELTZER P.S., S
CHANDRASEKHARAPPA S.C.;
                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                      JAG1.
                                                                                                                                                                                                                                                    EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                 JAGGED1.
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                 LLLALLC-ALRAKYCGASGQFELEILSMQNVNGELQNGNCCGGARNPGDRKCTRDECDTY
                                                                                                                                                                                    GENET. 0:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                   HNGGTCMNRVNSFECVCANGFRGKQC
                                                                                                                                                                                                                                                                                                                                                                                                                        QNGAQCYNRASDYFCKCPEDYEGKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPPGYAGDHCERDIDECASNPCLNGGHCQNEINRFQCLCPTGFSGNLCQLDIDYCEPNPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CVPGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSPNPCINGGSCQP-SGK--CICPAGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANGWSGKMCEEKVLTCSDKPC-HQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCE--HGHCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDYYYGFGCNKFCRPRDDFFGHYACDQNGNKTCMEGWMGPECNRAICRQGCSPKHGSCKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGGTCSNTGPDKYQCSCPEGYSGPNCEIAEHACLSD--PCHNRGSC-KE--TSLGFECEC
                                              h 27.4%;
Similarity 41.5%;
235; Conservative
                                                                                                                                                                                                                                                                                                          (TREMBLREL. 05,
(TREMBLREL. 05,
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                 MELTZER
                                               Pred.
                                                                                           MW;
                                                                                                                                                                                                         E B.L., C
                                              Score 1687; DB 2;
Pred. No. 0.00e+00;
110; Mismatches 192;
                                                                                                                                                                                                                                                                                                          CREATED)
LAST SEQUENCE UI
LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                VERTEBRATA;
                                                                                                                                                 P.S.,
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                                                                                           20F471DB
                                                                                                                                                                                                       OKAJIMA
R N.B., C
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                                                                                                                                                  CHANDRASEKHARAPPA
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                                                                                           CRC32;
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                                                                                                                                                                                                         COLLINS F.S.
                                                                                                                                                                                                                                                                TETRAPODA;
                                                                                                                                                                                                                                                                                                           UPDATE)
                                                                   Length 1218;
                                               Indels
                                                                                                                                                                                                                                                                MAMMALIA;
                                                                                                                                                                                                                  I.D.,
                                                                                                                                                  S.C.;
                                               29;
                                                                                                                                                                                                                    GENIN
                                               Gaps
    64
                        74
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DLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCE--HGHCDK 242
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CONFLICT 11
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Best Local S
Matches 23
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                                                                                                                           243 PNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRPCK 302
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                                                                                                                                                                                                                                                                                        303 NGGTCFNTGEGLYTCKCAPGYSGDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCHC 362
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                                        125 TFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTC 184
                                                                                                                                                                                  307
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                     SYTLLVEAW-DSSND-TVQPDSI-IEKASHSGMINPSRQWQTLKQNTGVAHFEYQIRVTC 187
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                                                                                                                                                                                    PGDCRCQYGWQGLYCDKCIPHPGCVHGICNEPWQCLCETNWGGQLCDKDLNYCGTHQPCL
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                                                                                                     DDYYYGFGCNKFCRPRDDFFGHYACDQNGNKTCMEGWMGRECNRAICRQGCSPKHGSCKL
                                                                                                                                                                                                                                                                   NGGTCSNTGPDKYQCSCPEGYSGPNCEIAEHACLSD--PCHNRGSC-KE--TSLGFECEC
                                                                                                                                                                                                                                                                                                                                                   363 SPGWTGPTCSTNIDDCSPNNCSHGGTCQD----L-VNG--FKCVCPPQWTGKTCQLDANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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Pred. No. 0.00e+00;
111; Mismatches 190; Indels
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TISSUB-SCIATIC NERVE;
MEDLINE; 95211842.
LINDSELL C.E., SHAMBER C.J., BOULTER J., WEINMASTER CELL 80:909-917(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, L38483; G1492111; -.
PROSITE, PS01187; BGF_CA; 8.
GLYCOPROTEIN: EGF-LIKE DOMAIN.
SEQUENCE 1219 AA; 134325 MW;
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Similarity 41.7%;
236; Conservative
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063722; P70640;
01-NOV-1996 (TREMBLREL. 0
01-FEB-1997 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
JAGGED PROTEIN.
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PGDCRCQYGWQGLYCDKCIPHPGCVHGTCNEPWQCLCETNWGGQLCDKDLNYCGTHQPCL 307
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Pred. No. 0.00e+00;
109; Mismatches 192; Indels 29; Gaps
                                                   243 PNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRPCK
                                                                                                                                                                                                                                                      NRGTCSNTGPDKYQCSCPEGYSGPNCEIAEHACLSD--PCHNRGSC-KE--TSSGFECEC
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EUTHERIA; PRIMATES.
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ZIMETH A.B., PEPPER M.S., MCMAHON G., NGUYEN F., MONTESANO R.,
MACIAG T.,
J. BIOL. CHEM. 271:32499-32502(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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ZIMRIN A.B., NGUYEN F., MACIAG T.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U77305; G1595274: -..
EMBL; U77720; E319096; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LI L., DENG Y., BANTA A.B., HOOD L.;
SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 95211842.
LINDSELL C.E., SHAWBER C.J., BOULTER J., WEINMASTER
CELL 80:909-917(1995).
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LAST SEQUENCE UPDATE)
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1227 AA; 134770 MW; 5D300B81 CRC32;
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01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATI
JAGGED 1 (TRANSMEMBRANE PROTEIN JAGGED).
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HNGGTCMNRVNSFECVCANGFRGKQC 564
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Local Similarity 41.7%;
nes 236; Conservative
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P78504 PRELIMINA
P78504;
01-MAY-1997 (TREMBLREL.
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RESULT 12
ID P79941;
AC P79941;
DT 01-MAY-1997 (
DT 01-MAY-1997 (
DT 01-JAN-1998 (
DE NOTCH LIGAND
GN X-DELTA-2.
CS XENOPUS LAEVI
OC EUKARXOTA; ME
RN [1]
RP SEQUENCE FROM
RA JEN W.C., WET
RL SUBMITTED (DE
DR EMBL; U70843;
DR PROSITE; PS011
KW GLYCOPROTEIN;
SQ SEQUENCE 644
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                                                                                                                                     Query Match
Best Local S
Matches 21
                                                                                                                                                                               SEQUENCE FROM N.A.

JEN W.C., METISTEIN D.A., CHITNIS A.B., KINT
JEN W.C., METISTEIN D.A., CHITNIS A.B., KINT
SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DA
EMBL; U70843; G1695891; -.
PROSITE; PS01186; EGF-Z; 7.
PROSITE; PS01187; EGF-CA; 2.
GLYCOPROTEIN; EGF-LIKE DOMAIN.
SEQUENCE 642 AA; 70667 MW; 2B0DDF2A CRC3
                                                                                                                                                                                                                                                                             X-DELTA-2.
X-DELTA-2.
XENOPUS LAEVIS (AFRICAN
XENOPUS LAEVIS (AFRICAN
XENARYOTA; METAZOA; CHO
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01-MAY-1997 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
NOTCH LIGAND X-DELTA-2.
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Similarity 44.5%;
216; Conservative
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                     Score 1648; DB 12;
Pred. No. 0.00e+00;
95; Mismatches 147;
                                                                                                                                                                                                                                                                                     VERTEBRATA;
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                                                                                                                                                                                   2B0DDF2A CRC32;
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Best Local S
Matches 23
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REMBL; D87558; D1022568; -.

R PROSITE; PS01187; EGF_CA; 8.

GLYCOPROTEIN; EGF-LIKE DOMAIN.

SEQUENCE 1212 x*
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O42347
O1-JAN-1998 (TREMBLREL. 0
O1-JAN-1998 (TREMBLREL. 0
O1-JAN-1998 (TREMBLREL. 0
O1-JAN-1998 (TREMBLREL. 0
C-SERRATE-2 (FRAGMENY).
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORD
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                        PDEYRCACPDGYSGKNCEIAEHAC-VS-NPCANGGTC-HE--ISSSFKCHCPSGWSGPTC
                                                                     AKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCE--HGHCDKPNQCVCQLG
                                                                                                                                                                                                                       DTTSQCTYGDVITPILGENSVNLTDAQRFQNKG-F--TNPIQFPFSFSWPGTFSLIVEAW
                                                                                                                                                                                                                                                                                                                 PTPAS
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l Similarity 41.8%;
233; Conservative
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102; M
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                         524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PAGAAGDRARARSRIGGHQDPGLVVIPFQFAWPRSFILIVEAW-DWDND-TIPDEELLIE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERAEHAC-AS-NPCANGGSC-HE--VLSGFECHCPSGWSGPTCALDIDECASNPCAAGGT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 AIDIDECASNPCAQGGTCID-H--INS----FECICPQQWIGATCQLDANECEGKPCVNA 405
                                          GRCCSGESDGA-TGKC-LGSCKTRFRVCLKHYQATIDTTSQCTYGDVITPILGENSVNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OYGNKACMDGWMGKECKEAVCKOGCNLLHGGCTVPGECRCSYGWGGKFCDECVPYPGCVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACCDGDGRTTRAGGCGRDECDTYVRVCLKEYQAKVTPTGPCSYGYGATPVLGSNSFYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVSHAGMINPEDRWKSLHFSGHVAHLELQIRVRCDENYYSATCNKFCRPRNDFFGHYTCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSCVEPWHCDCETNWGGLLCDKDLNYCGSHHPCVNGGTCINAEPDQYLCACPDGYLGKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C--VDQ-V----DGFECICPEQWVGATCQLDANECEGKPCLNAFSCKNLIGGYYCDCLPG
                                                                                                                                                                                                                                                           JAGGED2 (FRAGMENT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHBRIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1202;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SHAWBER C.J., BOULTER J., LINDSELL C.E., WEINMASTER G.
BEN BIOL. 1806.370-376(1996).
EMBL; U70050; G1718248; -.
PROSITE; PS01187; EGF_CA; 7.
GLYCOPROTEIN; EGF_LIKE DOMAIN.
NON_TER
                                                                                                                                                                                                                                    LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 24.5%; Score 1510; DB 10; Best Local Similarity 41.6%; Pred. No. 0.00e+00; Matches 225; Conservative 96; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                697F4205 CRC32;
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                                                                                                                                                                                                                            CREATED)
                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 1202 AA; 129704 MW;
                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                    525 GGDYYCACPDDYDGKNC 541
                                                                                                                                                  : | |:::|| |
548 VNSFECVCANGFRGKQC 564
                                                                                                                                                                                          114
P97607
P97607
P97607
P97607
01-MAY-1997 (TREMBLREL. 0:
01-MAY-1997 (TREMBLREL. 0:
01-JAN-1998 (TREMBLREL. 0:
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Gaps 17;
466 ICEDLVDGFRCHCPRGLSGPLCEVDVDLWCEPNPCLNGARCYNLEDDYYCACPEDFGGKN 525 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:5 | 505 TCLNLNNDYQCTCRAGFTGRDCSVDIDE-CŞSGPCHNGGTCMNRVNSFECVCANGFRGKO 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 YSQVNECLSNPCIHGNCTGGLSGYKCLCDAGWVGVNCEVDKNECLSNP-CQNGGTCNNLV 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 -PWTCICNEGWGGLYCNQDLNYCINHRPCKNGGTCFNTGEGLYTCKCAPGYSGDDCENEI 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 RPGLGSKGQGYQCECPIGYSGPNCDLQLDNCSPNPCINGGSC--QPSG-KCICPAGFSGT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 NGYRCTCKKGFKGYNCQVNIDECASN-PCLNQGTCFDDVSG-YTCHCMLPYTGKNCQTVL 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 APCSP--NPCENAAVCKEAPNFES-FSCLCAPGWQGKRCTVDVDECISKPCMNNGVCHNT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q---GS----YVCECPPGFSGMDCEEDINDCLANPCQNGGSCVDHVNTFSCQCHPGFIGD 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KCQTDMNECLSEPCKNGGTCSDYVNSYTCTCPAGFHGVHCENNIDECTESSCFNGGTCVD 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GINSFSCLCPVGFTGPFCLHDINECSSNPCLNAGTCVDGLGTYRCICPLGYTGKNCQ 744
                                                                                                                                                                                                                                                                                                                                                                                      MOTCHE OR MOTCH B.
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 970; DB 10; Length 1203;
Pred. No. 2.11e-195;
74; Mismatches 108; Indels 29;
                                                                                                                                                                                                                                                                                              01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
NOTCH PROTEIN HOMOLOG 2 (MOTCH B PROTEIN) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAINET (CBA X C57BL); TISSUB-WHOLE EMBRXO;
STRAINES; 93178563.
LARDELLI M., LENDAHL U.;
EXP. CELL RES. 204:364-372(1993).
EXP. CELL RES. 204:364-372(1993).
MGD; MGI:977364; NOTCH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 1 1203 1203
NON_TER 1203 1203
SEQUENCE 1203 AA; 128982 MW; A5A95551 CRC32;
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ne : 163 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIFFERENTIATION; NEUROGENESIS; REPEAT
                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match
Local Similarity 40.9%;
nes 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; RODENTIA.
                                                                                                     526 C 526
                                                                                                                                                  564 C 564
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Q06008
Q06008;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Jun 12 12:02:18 1998;

Tabular output not generated. MasPar time 7.48 Seconds 471.739 Million cell upd updates/sec

Title: Sequence: Description: Perfect Score: >US-08-083-590A-2 (1-230) from US08083590A.pep (2 of 2) 1734 1 MHWIKCLLTAFICFTVIVQV.....ETGEIICLTGWQGDYCHIPK 230

Searched: Scoring table: PAM 150 Gap 11 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31-2

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 31.938; Variance 122.652; scale 0.260

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 7 9 9 10 11 12 13 13 14 15 16 16 | 654321 | Result |
|--|--|-----------------------|
| 729 727 727 590 574 574 571 571 486 486 429 | 1734 1734 775 775 775 751 732 | Score |
| 42.0 41.9 34.0 33.1 33.1 33.1 27.9 27.9 24.7 | | Query Match Length |
| | 236 7 833 6 727 21 740 21 723 25 722 21 | Length DB |
| | 7 R38305 6 R2896C 6 W11719 1 W10876 1 W00876 1 W18353 | B |
| proliferation and proliferation and proliferation and Human Serrate-1 (Proliferation and Proliferation and Proliferation and Proliferation and Proliferation and Proliferation and Chick Serrate. Proliferation and Sequence of a ser Serrate protein. H-Delta-1 polypep H-Delta-1 polypep | Sequence of a del Delta D11. C-Delta-1 polypep C-Delta-1 polypep Proliferation and M-Delta-1 polypep | Description |
| A A (7 (3 N) N D D (3 N) (3 N) N | 2.83e-176 2.83e-176 2.25e-70 2.25e-70 2.25e-70 9.25e-68 1.08e-65 | Pred. No. |

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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 2 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
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| 83 | 83 | 83 | 83 | 86 | 87 | 87 | 87 | 87 | 87 | 86 | 89 | 88 | 88 | 89 | 92 | 92 | 92 | 94 | 95 | 97 | 101 | 100 | 139 | 206 | 260 |
| 4.8 | 4.8 | 4.8 | 4.8 | | 5.0 | | 5.0 | | 5.0 | 5.0 | | 5.1 | | 5.1 | | 5.3 | | 5.4 | 5.5 | 5.6 | 5.8 | | | 11.9 | 15.0 |
| 2199 | 1833 | 1124 | 1124 | | | | | | 271 | | | 316 | | | 768 | 768 | 751 | 969 | 385 | 557 | 788 | | | | 1257 |
| 16 | 14 | 9 | 14 | 16 | 10 | 21 | 21 | 1 | 10 | 23 | 21 | 11 | 11 | 21 | G | G | 21 | œ | 10 | տ | ហ | 10 | 19 | 25 | 19 |
| R94562 | R79478 | R45440 | R73953 | R94563 | R51500 | W13573 | W13574 | R05936 | R51070 | W25965 | W20678 | R57058 | R57062 | W20370 | R27684 | R27683 | W01825 | R41662 | R56167 | R26323 | R26322 | R56166 | W05836 | W18346 | W05834 |
| Human cytotactin. | • | Human orphan receptor | Human TEK tyrosine ki | Chicken cytotactin. | Human platelet GPIIIa | Mouse beta-3 integrin | Mouse beta-3 integrin | Secreted GPIIIa subun | A water channel prote | ORF 5 protein of PRRS | H. pylori transporter | P. aeruginosa mucB. | = | H. pylori transporter | Human beta-8 intergin | Rabbit beta-8 intergi | Human metalloproteina | Paired basic amino ac | Neuroendocrine tumor | B6GP. | в6н. | Neuroendocrine tumor | Mouse M-Serrate-1 (DS | Proliferation and dif | Human Serrate-2 (HJ2) |
| 4.57e+01 | 4.57e+01 | 4.57e+01 | 4.57e+01 | 2.67e+01 | 2.23e+01 | 2.23e+01 | 2.23e+01 | 2.23e+01 | 2.23e+01 | 2.67e+01 | 1.55e+01 | 1.86e+01 | 1.86e+01 | 1.55e+01 | 8.93e+00 | 8.93e+00 | 8.93e+00 | 6.16e+00 | 5.11e+00 | 3.51e+00 | 1.64e+00 | | 7.82e-04 | 3.42e-10 | 1.42e-15 |

ALIGNMENTS

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RESULT
ID R3
AC R.
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                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                purified serrate protein, nucleic acid and antibodies - used in the study and manipulation of differentiation and other physiological processes
Disclosure; Page 85; 119pp; English.
Delta encodes an approx. 100 kd protein (Delta denotes 'DLZM', the protein product of the predominant zygotic and maternal transcripts) that has nine EGF-like repeats within its extracellular domain. Molecular studies have lead to the suggestion that Notch and Delta constitute biochemically interacting elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-1993 (first entry)
Sequence of a delta protein.
Delta; toporythmic protein; family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
WO9312141-A.
                                                                                                                                                                                                                                                                                                                   of a cell communication mechanism involved in early developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; Q43911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 93-214095/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R38305 standard; Protein; R38305;
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                   decisions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Artavanis-tsakonas S, Fleming RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYYA ) UNIV YALE.
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121
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                                                                                       61 cktrfrvclkhygatidttsqctygdvitpilgensvnltdagrfqnkgftnpiqfpfsf 120
                                                                                                                                          \vdash
                                                                                                                                                            1 mhwikclltaficftvivqvhssgsfelrlkyfsndhgrdnegrccsgesdgatgkclgs 60
                swpgtfsliveawhdtnnsgnartnklliqrllvqqvlevssewktnksesqytsleydf 180
SWPGTFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDF 180
                                                                   CKTRFRVCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSF 120
                                                                                                                                          MHWIKCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGS 60
                                                                                                                                                                                                                                                                                  236 AA;
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                                                                                                                                                                                                         Score 1734; DB 7;
Pred. No. 2.83e-176;
0; Mismatches 0;
                                                                                                                                                                                                                                            Length 236;
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colon cancer; melanoma; seminoma;

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lung cancer; c
neurogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and manipulation of differentiation processes
(laim 50; Fig 13; 239p; English.
The sequence given is encoded by the nucleotide sequence of human
Delta gene contained in plasmid cDNA clone Dil. A human expression
Library was constructed and screening assays were carried out on to
select for the expressed Delta product. Alternatively the sequences
could be isolated by amplification using polymerase chain reaction
(PCR) primers. The isolated gene may be inserted into a cloning
vector and expressed. The Delta gene and also the Notch and Serrate
neurogenic genes are designated 'toporythmic' genes. The proteins
they encode are involved in specific homo- or heterotypic interactions
crucial to differentiation. The quantitation of mRNA for human Notch
possible using the DNA and antibodies raised against the Notch and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 cktrfrvclkhygatidttsgctygdvitpilgensvnltdagrfgnkgftnpidfpfsf 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 mhwikclltaficftvivqvhssgsfelrlkyfsndhgrdnegrccsgesdgatgkclgs 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                 Human; Notch; plasmid; cDNA; clone; D11; expression library; PCR;
POJYmerase chain reaction; primer; cloning vector; Delta; Serrate;
neurogenic; toporythmic; homotypic; heterotypic; differentiation;
quantitation; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Notch and Delta DNA and protein sequences - used for study
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Artavanis-Tsakonas S, Blaumueller CM, Fehon RG, Muskavitch MAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1734; DB 6; Length 833; Pred. No. 2.83e-176;
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W11719;
28-APR-1997 (first entry)
C-Delta-1 polypeptide.
C-Delta-1; cell proliferation; nervous system disorder; tissue regeneration; Notch; cervix cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                    rvtcdlnyygsgcakfcrprddsfghstcsetgeiicltgwggdychipk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                   Ź
                                                                                                                          T 2
R28960 standard; Protein; 833
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01-MAY-1992; U03651:
03-MAY-1991; US-695189.
14-NOV-1991; US-791923.
(INDV ) UNIV INDIANA FOUND.
(UXYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                           01-APR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rebay I, Shepard SB;
WPI; 92-398861/48.
N-PSDB; Q30997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  833 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delta proteins
Sequence 833
                                                                                                                                                                                                                                                                                                                      Homo sapiens.
WO9219734-A.
                                                                                                                                                                                                                                                                                                                                                                12-NOV-1992
                                                                                                                                                                                                                 Delta Dil
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                                                                                                                                                                     R28960;
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                    181
                                                                                                                               RESULT
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regeneration

Spisclosure; Fig 2; 135pp; English.

C-delta-1 polypeptide (W1119) is the chick homologue of Drosophila C-delta-1 polypeptide (W1119) is the chick homologue of Drosophila Delta, a protein that binds to Notch protein. Expression of C-delta-1 correlates with onset of neurogenesis. The C-delta-1 cannon acid sequence was deduced from a cDNA clone (T58897) obtd.

C rom chick stage 4-6 embryos. An alternatively spliced variant of From chick stage 4-6 embryos. An alternatively spliced variant of From 1979peptides have been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, and nervous system disorders or to Sequence 727 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 ddlttenperlisrlatgrhlavgeewsqdlhssgrtdlkysyrfvcdehyygegcsvfc 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 qvdgsgvfelklqefvnkkgllsnrnccrgggpggagqqqdcktffrvclkhyqasvsp 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New vertebrate Delta protein, DNA and antibodies - for treating and preventing cancer, nervous system disorders and for tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 OVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFRVCLKHYQATIDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Mismatches 74; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 775; DB 21;
Pred. No. 2.25e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Henrique D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 RPRDDSFGHSTCSETGEIICLTGWQGDYCHIP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 rprddrfghftcgergekvcnpgwkgqyctep 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                      486..523
/label= EGF8
524..534
                                                                                                                                                                                                                                                                                                                      EGF5
                                                                                                                                                                                                                                                                                                                                                                   /label= EGF6
                                                                                                             229..261
/label= EGF1
                                                                                                                                                                                   /label= EGF2
                                                                                                                                                                                                                                /label= EGF3
                                                                                                                                                                                                                                                                           /label= EGF4
                                                                                                                                                                                                                                                                                                                                                                                                                 /label= EGF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= EGF9
                                                                                      /label= DSL
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Best Local Similarity 49.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- TM
                                                                                                                                                                                                                                                                                         3/1..409
/label= FC
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                                                                                                                                                                                                      .332
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                                                                                                                                                        262..292
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therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 011178
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28-JUN-1996;
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Best Local :
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                                                                                                   C-Delta-1 correlates with onset of neurogenesis. The C-delta-1 amino acid sequence was deduced from a cDNA clone (T58898) obtd. from chick stage 4-6 embryos. A shorter version (W58877) of C-Delta-1, lacking the 12 C-terminal amino acids of the longer version, was also isolated, and mouse (W11720) and human (W11721-38) Delta-1 polyapptides have been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, and nervous system disorders or to promote tissue regeneration and repair.
                                                                                                                                                                                                                                                             N-PSDB; T58898.
New vertebrate Delta protein, DNA and antibodies -
                                                                                                                                                                                                                        Disclosure; Fig 2; 135pp; English.
C-delta-1 polypeptide (W00876) is the chick homologue of Drosophila Delta, a protein that binds to Notch protein. Expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-Delta-1; cell proliferation; nervous system disorder; tissue regeneration; Notch; cervix cancer; breast cance lung cancer; colon cancer; melanoma, comitation.
                                                                                                                                                                                                                                                                                                                                  16-JAN-1997.
28-JUN-1996; U11178.
28-JUN-1995; US-000589.
(IMCR ) IMPERIAL CANCER RES
(UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                            regeneration
                                                                                                                                                                                                                                                                                                               Lewis
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                               eppctygsaitpvlgansfsvpdgaggadpafsnpirfpfgftwpgtfsliiealhtdsp 139
                       QVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFRVCLKHYQATIDT 78
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                                                                          Similarity
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555..579
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524..534
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486..52
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229..261
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                                                              Score 775; DB 21;
Pred. No. 2.25e-70;
33; Mismatches 74
                                                                                                                                                                                                                                                                                                                          GE,
                                                                                                                                                                                                                                                                                                                                               TECHNOLOGY
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                                                                                                                                                                                                                                                                                                                          Henrique D,
                                                               74;
                                                                                                                                                                                                                                                                                                                          Ish-Horowicz
                                                                                                                                                                                                                                                                       for
                                                                                   Length 740;
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Best Local Similarity 46.5%;
                           W11720 standa
W11720;
28-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as neurons and blood cells. The polypeptide may be used for th prevention and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement blood formation, e.g. after immunosuppression.

Sequence 723 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 5
W18353
      M-Delta-1
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serrate-1; blood cell; neuron; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W18353;
11-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells suppressed to the contract of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide(s) encoded by human genes delta-1 and serrate-1 proliferation and differentiation of undifferentiated h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-1997.
15-NOV-1996; J03356.
30-NOV-1995; JP-311811.
17-NOV-1995; JP-299611.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Itoh A, Sakano S; WPI; 97-298110/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASAH ) ASAHI KASEI KOGYO
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                                                                                                    standard;
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polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 77-82; 114pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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22..723
/label=
                                                                                                    Protein;
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differentiation suppression polypeptide.
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Pred. No. 9.
39; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 25; I
).25e-68;
ches 76;
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Homo sapiens.
WO9719172-A1.
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د
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                                                                                                                                                                                                                                                                                                                                                                                                                                       14 allcqvwssgvfelklqefvnkkgllgnrnccrggs-gpp--c--acrtffrvclkhyqa 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 TVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFRVCLKHYQA 74
                                                                                                                                                                                                                             Claim 4: Fig 8: 135pp; English.

M-delta-1 polypeptide (W11720) is the mouse homologue of Drosophila Delta-1 a protein that binds to Notch protein. It is expressed primarily in presomitic mesoderm, the central and peripheral nervous systems, and kidney. Chick (W11719) and human (W11721-38) Delta-1 polypeptides have also been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, as well as nervous system disorders, sequence 722 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               7; Gaps
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                                                                                                                                                                                             treating
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The present sequence represents a polypeptide which suppresses
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                                                                                                                                                                                                                                                                                                                                                                                   Score 732; DB 21; Length 722;
Pred. No. 1.08e-65;
38; Mismatches 68; Indels
                                                                                                                                            Ish-Horowicz
                                                                                                                                                                                            New vertebrate Delta protein, DNA and antibodies - for tree preventing cancer, nervous system disorders and for tissue
M-Delta-1; cell proliferation; nervous system disorder; tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer; colon cancer; melanoma; seminoma;
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                                                                                                28-JUN-1995; US-000589.
(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
(UYYA ) UNIV YALE.
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                                                                                                                                           Gray GE,
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15-MOV-1996, J03356.
30-MOV-1995, JP-311811.
17-NOV-1995, JP-299611.
(ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 47.7%;
Matches 103; Conservative
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11-FEB-1998 (first entry)
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                                                                                                                                           Artavanis-Tsakonas S,
                                         neurogenesis; therapy
                                                                                16-JAN-1997.
28-JUN-1996; Ulll78.
                                                                                                                                                     Lewis J;
wpI: 97-100159/09.
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WPI; 97-298110/27
                                                                                                                                                                                 N-PSDB; T58899
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                                                      Mus sp.
WO9701571-A1.
                                                                                                                                                                                                                      regeneration
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                                                                              16-JAN-1997
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57 tygsavtpvlgvdsfslpdggg-adsafsnpirfpfgftwpgtfsliiealhtdspddla 115
||| :||:|| :| :| :| :| :
83 TYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWPGTFSLIVEAWH-DINNSGN 141
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                                                                                                                                                                                                                                                                                                                           1 sgvfelklqefvnkkgllgnrnccrgga-gppp-c--acrtffrvclkhyqasvspeppc 56
                                                                                                                                                                                                                                                                                                                                                                                  23 SGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFRVCLKHYQATIDTTSQC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement oblood formation, e.g. after immunosuppression.
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9
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                                                                                                                                                                                                            Length 520;
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                                                                                                                                                                                                   Score 729; DB 25; Length 52(
Pred. No. 2.29e-65;
33; Mismatches 69; Indels
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Pred. No. 2.29e-65;
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W18349 standard; protein; 702
W18349;
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15-WOV-1995, J03356.
17-WOV-1995, JP-311811.
17-WOV-1995, JP-299611.
(ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                                                                                                   Query Match
Best Local Similarity 48.1%;
Matches 100; Conservative
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Best Local Similarity 48.1%;
Matches 100; Conservative
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WPI; 97-298110/27
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Best Local S
Matches
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15-NOV-1996; J03356.
30-NOV-1995; JP-311811.
17-NOV-1995; JP-299611.
(ASAH) ASAHI KASEI KOGYO K
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W05833 standard;
W05833;
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Proliferation and differentiation suppression polypeptide.
Proliferation; differentiation; suppression; human; delta-1;
serrate-1; blood cell; neuron; leukaemia; malignant tumour;
                                                                                                                                                              diagnosis; antibody
                                                                                                                                                                             Serrate-1; human jagged-1; cell fate; central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prooq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide(s) encoded by human genes proliferation and differentiation
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WPI; 97-298110/27
                                                                                   peptide
                                                                                                                 domain
                                                                                                                                                Homo
                                                                                                                                                                                                             Human
                                                                                                                                                                                                                          28-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W18347;
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                                                                                                                                                sapiens.
                                                                                                                                                                                                                                                                                                                                     dafghftcgergekvcnpgwkgpyc
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|:||| ||:| || || || ||
                                                                                                                                                                                                                                                                                                                     DSFGHSTCSETGELICLTGWQGDYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFRVCLKHYQATIDTTSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
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                                                                                                                                                                                                           Serrate-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                formation, e.g. after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tion and control of disorders involving undifferentiated such as leukaemia and malignant tumours, and improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 48.3%, 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 AA;
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57-58; 114pp;
                                                   /label=
185..229
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/label- DSL
/note- "region of homology with Drosophila
and Serrate, predicted to mediate binding
                                                                                                                              Location/Qualifiers
                                                                                                 /label-
                                                                                                                                                                                                                                                          Protein;
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                                                      229
                                                                   Sig_peptide
                                                                                                 Extracellular_domain
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                                                                                                                                                                             HJ1; Notch; cell differentiation; system; cancer; tissue repair; th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 727; DB 25;
Pred. No. 3.78e-65;
33; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppression.
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  of undifferentiated human blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
                                                                                                                                                                             cancer; tissue repair; therapy;
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                        Delta
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                                                      prevent malignancies characterised by increased Notch activity.

PS Claim 4; Page 95-98; 161pp; English.

CC Human Serrate-1 (W0583) and human Serrate-2 (W0583) are ligands

CC for the zygotic neurogenic locus Notch, and are believed to play a

CC major role in determining cell fates (differentiation) in the

CC central nervous system. Their amino acid sequences were deduced

CC from CDNA clones (see also T40090-91) isolated from human foetal

CC brain cDNA libraries. The proteins, antibodies raised to them,

CC and encoding nucleic acids can be used in the detection of

CS errate sequences and in the treatment of disorders of cell fate

CC and in tissue repair or regeneration
   Query Match
Best Local Similarity
                                                   and in ti
Sequence
                                                                                                                                                                                                                                                                                                                                                  12-SEP-1996.
07-MAR-1996; U03172.
07-MAR-1995; US-400159.
(IMCR ) IMPERIAL CANCER
                                                                                                                                                                                                                                                                        N-PSDB; T40090.
                                                                                                                                                                                                                                                                                                     Lewis
                                                                                                                                                                                                                                                                                                                     Artavanis-Tsakonas S,
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96-425379/42.
                                                    tissue repair
ce 1218 AA;
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/label- int
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/note- "epidermal growth factor-like repeat domain"
234..264
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        34.0%;
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Myat AM;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Intracellular_domain
                                                                                                                                                                                                                                                                                                                     Œ,
        Score 590; DB 19;
Pred. No. 2.58e-50;
                                                                                                                                                                                                                                                                                                                     Henrique
                                                                                                                                                                                                                                                                                                                       DMP,
                    Length
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                        1218;
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Matches

131

188

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The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as leukamia and malignant tumours, and improvement of blood formation, e.g. after immunosuppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                itoh A, Sakano S;
WPI: 97-298110/27.
Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress
proliferation and differentiation of undifferentiated human blood
cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 SGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCL-GSCKTRFRVCLKHYQATIDTTSQ
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                                                                                                       Proliferation and differentiation suppression polypeptide. Proliferation; differentiation; suppression; human; delta-1; serrate-1; blood cell; neuron; leukaemia; malignant tumour; immunosuppression.
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                                                                                                                                                                                                                                                                                                                     itoh A, Sakano S;
WPI; 97-298110/27.
Peptide(s) encoded by human genes delta-1 and serrate-1 - su
proliferation and differentiation of undifferentiated human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 574; DB 25;
Pred. No. 1.36e-48;
47; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 66-71; 114pp; Japanese
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                                                     standard; protein; 1036 AA
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30-NOV-1995; JP-311811.
17-NOV-1995; JP-299611.
(ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                                                                                                                                                                                                     (ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.1%;
Local Similarity 39.3%;
hes 81; Conservative
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30-NOV-1995; JP-311811.
17-NOV-1995; JP-299611.
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WO9719172-A1.
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WO9719172-A1.
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                                                                                                               fkvclkeygsrvtaggpcsfgsgstpviggntfnlkas-r-gn-d-pnrivlpfsfawpr 130
                                                                                                                                   sytllveaw-dssnd-tvqpdsi-iekashsgminpsrqwqtlkqntgvahfeyqirvtc 187
                                                                                                                                                                                                             sytllveaw-dssnd-tvqpdsi-iekashsgminpsrqwqtlkqntgvahfeyqirvtc 187
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Gaps
                                   16 lllallc-alrakvcgasggfeleilsmgnvngelgngnccggarnpgdrkctrdecdty 74
                                                           111allc-alrakvcgasgqfeleilsmqnvngelqngnccggarnpgdrkctrdecdty 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress proliferation and differentiation of undifferentiated human blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 579; DB 25; Length 1218;
Pred. No. 3.94e-49;
52; Mismatches 76; Indels 10;
Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Proliferation and differentiation suppression polypeptide. Proliferation; differentiation; suppression; human; delta-1; serrate-1; blood cell; neuron; leukaemia; malignant tumour; Immunosuppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32..1218 // Alabel Differentiation_suppression_protein
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                                                                                                                                                                                                                                                                   ddyyygfgcnkfcrprddffghyacdqngnktcmegwmgpecn 230
                                                                                                                                                                                                                                                                                       185 DLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCH 227
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16;
50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 83-91; 114pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               л 11
W18354 standard; protein; 1218 АА.
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/label= Signal
32..1218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.4%;
Best Local Similarity 38.1%;
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   W18354;
11-FEB-1998 (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-NOV-1996; J03356.
30-NOV-1995; JP-311811.
17-NOV-1995; JP-299611.
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87;
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Gaps

Length 1036; Indels

- suppress man blood

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Query Match
Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                             Chick Serrate.
C-Serrate; Notch; cell differentiation;
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 /label=
541..606
/label=
607..644
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352..390
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                                            503..
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208..2
                                                                  465..
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                                                                                                                                                                                                                                                                                                                /label= Sig_peptide
/note= "lacks the N-terminal portion owing truncation of the encoding cDNA clone"
                                                      /label=
                                                                                                                                                                                                                                                                      /note= "region of homology with Drosophila
and Serrate, predicted to mediate binding
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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Pred. No. 1.36e-48;
47; Mismatches 70;
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 Homo sapiens.

W09719172-A1.

29-MAY-1997.

15-NOV-1996; J03356.

30-NOV-1995; JP-311811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP 1996. U03172. 
07-MAR-1995; US-400159. 
(IMCR) IMPERIAL CANCER R 
(UYYA) UNIV YALE. 
Artavanis-Tsakonas S, Gr
                                                                                                                                                                                                                                                                                                                                                                           Vertebrate Serrate protein and related DNA - used to treat or prevent malignancies characterised by increased Notch activity. Disclosure; Page 112-115; 161pp; English.
Chicken Serrate (W05835), or C-Serrate, is a ligand for the zygo neurogenic locus Notch and is believed to play a major role in determining cell fates in the central nervous system. Its amino acid sequence was deduced from a cDNA clone (T40092) obtd. from optic explant cDNA library. C-Serrate is expressed in the central nervous system, cranial placodes, nephric mesoderm, vascular system, and limb bud mesenchyme.
Sequence 1193 AA;
                                                              Proliferation and differentiation suppression polypeptide Proliferation; differentiation; suppression; human; delta serrate-1; blood cell; neuron; leukaemia; malignant tumous
                                                                                                                  NT 15
W18350 standard; protein;
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84; Conser
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llarity 39.8%;
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1067..1193
/label= Intracellular_domain
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1. No. 2.86e-48;
Mismatches 71;
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                                                                                                                                                               227
                                                                                                                                                                                    204
                                                                  malignant tumour;
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The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement of blood formation, e.g. after immunosuppression.
17-NOV-1995; JP-299611.

(ASAH) ASAHI KASEI KOGYO KK.

HICH A, Sakano 3;

WPI; 97-298110/27.

Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress proliferation and differentiation of undifferentiated human blood cells

Claim 2; Page 65-66; 114pp; Japanese.
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9 1 sgqfeleilsmgnvngelqngnccggarnpgdrkctrdecdtyfkvclkeygsrvtaggp 60 8; Gaps Score 544; DB 25; Length 192; Pred. No. 2.27e-45; 46; Mismatches 67; Indels Query Match 31.4%; Best Local Similarity 39.2%; Matches 78; Conservative

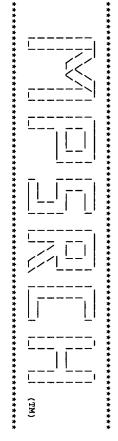
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23 SGSFELRLKYFSNDHGRDNBGRCCSGESDGATGKCL-GSCKTRFRVCLKHYQATIDITSQ 81

174 dffghyacdqngnktcmeg 192 | ||| :| : |: |

202 DSFGHSTCSETGEIICLTG 220

Search completed: Fri Jun 12 12:03:36 1998 Job time : 78 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 12 12:06:43 1998; MasPar time 2.40 Seconds 549.166 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-083-590A-2 (1-230) from US08083590A.pep (2 of 2) 1734

1 MHWIKCLLTAFICFTVIVQV......ETGEIICLTGWQGDYCHIPK 230

Scoring table: PAM 150 Gap 11

Searched: 62624 seqs, 5720858 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 30.190; Variance 125.451; scale 0.241

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | œ | 7 | σ | 5 | 4 | ω | 2 | 1 | No. | Result |
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| 82 | 83 | 83 | 83 | 83 | 86 | 87 | 87 | 87 | 88 | 88 | 88 | 92 | 92 | 94 | 95 | 95 | 100 | 100 | 452 | 480 | 1514 | 1734 | Score | |
| 4.7 | 80 | 4.8 | 4.8 | 4.8 | 5.0 | 5.0 | 5.0 | 5.0 | 5.1 | 5.1 | 5.1 | 5.3 | 5. 3 | | | 5.5 | | 5.8 | 26.1 | 27.7 | 87.3 | 100.0 | | Query |
| . 283 | 2199 | 1833 | 1124 | 1124 | 1810 | 718 | 718 | 271 | 316 | 316 | 316 | 769 | 768 | 969 | 385 | 385 | 383 | 383 | 199 | 293 | 203 | 833 | Length I | |
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| US-08-658- | PCT-US95-1 | PCT-US95-0 | US-08-323- | PCT-US93-0 | PCT-US95-1 | US-08-445- | US-08-444- | US-08-447- | US-08-017- | PCT-US94-0 | US-08-260- | US-08-454- | US-08-454- | PCT-US93-0 | US-08-457- | us-08-597- | us-08-597- | US-08-457- | US-08-264- | US-08-264- | US-08-264- | US-08-264- | Ħ | |
| Sequence | | Sequence | Sequence | Sequence | Sequence | Sequence | Description | |
| 2, | 2 | 18. | , | 'n | 4, | 4, | 4, | 4 | 18, | 18, | 18, | 6 | 4, | 2, | , | ۳, | 2, | 2 | 4. | 9 | ω, | 6 | B | |
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| 2.61e+01 | 2.21e+01 | • | 2.21e+01 | 2.21e+01 | 1.32e+01 | 1.11e+01 | 1.11e+01 | 1.11e+01 | 9.36e+00 | 9.36e+00 | 9.36e+00 | 4.65e+00 | 4.65e+00 | 3.26e+00 | 2.73e+00 | 2.73e+00 | 1.11e+00 | 1.11e+00 | 1.84e-33 | 3.16e-36 | 3.50e-141 | 8.30e-164 | Pred. No. | |

| | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 5 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 |
|--------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-----------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|--------------|-------------|-------------|-------------|-------------|-------------|-------------|
| | 77 | 77 | 77 | 78 | 78 | 78 | 78 | 78 | 79 | 79 | 79 | 79 | 79 | 79 | 79 | 79 | 81 | 81 | 81 | 81 | 81 | 18 |
| | 4.4 | 4.4 | 4.4 | 4.5 | 4.5 | 4.5 | 4.5 | 4.5 | 4.6 | 4.6 | 4.6 | 4.6 | 4.6 | 4.6 | 4.6 | 4.6 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 |
| | 336 | 336 | 47 | 541 | 501 | 501 | 501 | 501 | 769 | 769 | 769 | 688 | 670 | 670 | 670 | 650 | 1358 | 1358 | 1358 | 925 | 464 | 416 |
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| AT TOWNSHIPS | US-07-704- | US-08-093- | US-08-377- | PCT-US95-0 | US-08-271- | US-07-687- | US-08-434- | 5168064-4 | US-08-477- | US-08-243- | US-08-484- | US-08-325- | US-08-484- | US-08-243- | US-08-477- | US-08-325- | US-08-404- | US-08-404- | US-08-404- | US-08-252- | US-08-252- | us-08-252- |
| • | Sequence 3, | Sequence 2, | Sequence 30 | Sequence 2, | Sequence 2, | Sequence 2, | Sequence 2, | ٠ | Sequence 4, | Sequence 4, | Sequence 4, | Sequence 57 | Sequence 3, | Sequence 3, | Sequence 3, | Sequence 56, | Sequence 4, | Sequence 4, | Sequence 4, | Sequence 4, | Sequence 6, | Sequence 2, |
| | Applicatio | Applicatio | , Applicati | Applicatio | Applicatio | Applicatio | Applicatio | 5168064. | Applicatio | | ~ | , Applicati | Applicatio | Applicatio | ~ | , Applicati | Applicatio | Applicatio | Applicatio | Applicatio | Applicatio | Applicatio |
| | 6.02e+01 | 6.02e+01 | 6.02e+01 | 5.11e+01 | 5.11e+01 | 5.11e+01 | 5.11e+01 | 5.11e+01 | 4.33e+01 | 3.10e+01 | 3.10e+01 | 3.10e+01 | 3.10e+01 | 3.10e+01 | 3.10e+01 |
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ALIGNMENTS

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| amino acid | LENGTH: 833 amino acids | SEQUENCE CHARACTERISTICS: | INFORMATION FOR SEQ ID NO: 6: | TELEX: 66141 PENNIE | TELEFAX: 212 8698864/9741 | | TELECOMMUNICATION INFORMATION: | | è | NAME: Misrock, S. Leslie | ATTORNEY/AGENT INFORMATION: | FILING DATE: 03-MAY-1991 | APPLICATION NUMBER: US 07/695,189 | PRIOR APPLICATION DATA: | CLASSIFICATION: 435 | | APPLICATION NUMBER: US/08/264,534 | LICATION DATA: | | 'n | COMPUTER: IBM PC compatible | MEDIUM TYPE: Floppy disk | | | ĸ | STATE: New York | New York | 5 Avenue | ADDRESSEE: Pennie & Edmonds | CORRESPONDENCE ADDRESS: | R OF SEQUENCES: 34 | OF INVENTION: In Toporythmic Proteins, And Methods Ba | | nis-Tsakonas | GENERAL TINEORMATION: | | Sequence 6. Application US/08264534 | | Sequence 6, Application US/08264534. | | 01-JAN-1900 | | XXXXX | 05-00-204-334-0 SIMNUARU; FRI; 633 RA. | 1 1 1 C-00-364-534-6 CTANDADD. DDT. 033 |

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01-JAN-1900
                  SEQUENCE
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                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08264534
Patent No. 5648464
GENERAL INFORMATION:
APPLICANT: Attavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains
TITLE OF INVENTION: IN TOPOTYTHMIC Proteins, And Methods Based Thereon NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                      ö
                                                                                                          121 SWPGTFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDF 180
                                                                                                                                                         1 MHWIKCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGS 60
                                                       Gaps
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                                                                                                                                                                                    RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPK 230
                                                                                                                                                                                              181 RVICDLNYYGSGCAKFCRPRDDSFGHSTCSETGELICLFGWGGDYCHIPK 230
                                     Length 833;
                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,534
FILING DATE:
                                   Score 1734; DB 1; I
Pred. No. 8.30e-164;
0; Mismatches 0;
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                                                                                                                                                                                                                                         203
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REGISTRATION NUMBER: 18,872
RELECOMMUNICATION NUMBER: 7326-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPK: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,189
FILING DATE: 03-MAX-1991
ATTORNEY/AGENT INFORMATION:
TOPOLOGY: unknown
MOLECULE TYPE: protein
JENCE 833 AA; 88812 MW; 3155492 CN;
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08264534.
                                                                                                                                                                                                                                          STANDARD;
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                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 230; Conservative
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                  SEQUENCE
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Sequence 9, Application US/08264534
Patent No. 5648464
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                      61 YGDVITPILGENSVNLTDAQRFQNKGFINPIQFPFSFSWPGTFSLIVEAWHDTNNSGNAR 120
                                                                                                                                                                                                                                                                                                               121 TNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTCDLNYYGSGCAKFCRPRDDS 180
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                                                                                                                                                                                                                14 GSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFRVCLKHYQATIDITSQCT 83
                                                                                                                                                                                          1 GSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFRVCLKHYQATIDTTSQCT 60
                                                                                                                                             Gaps
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                                                                                              Length 203;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,534
FILING DATE:
                                                                                           Score 1514; DB 1; I
Pred. No. 3.50e-141;
0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,189
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CONTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FENCE 203 AA; 22840 MW; 218129 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08264534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 FGHSTCSETGELICLTGWQGDYC 203
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                                                                                         Match 87.3%;
Local Similarity 100.0%;
les 203; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08264534 Patent No. 5648464
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                                                              INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
                                                  SEQUENCE CHARACTERISTICS:
                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 212 790-9090
                                                                                                                                               APPLICATION NUMBER: US 07/695,189
FILING DATE: 03-MAY-1991
ATTORNEY_ACENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRERVCLKHYQATID-TT-SQ-CTYGDVITPILGENSVNLTDAQREQNKGFTNPIQEPES 119
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                                                                       TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                         REGISTRATION NUMBER: 18
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
                                      LENGTH:
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ilarity 36.1%;
Conservative
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                                    199 amino acids
                                                                                                                                                                                                                                                                                                                                                                      1155 Avenue of the Americas
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TENTION: Human No. 5648464ch And Delta, Binding Domains
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32286 MW; 438798 CN;
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               single
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                                                                                                                                   18,872
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Pred. No. 3.16e-36;
59; Mismatches 70;
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Best Local Similarity
77; Conserv
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   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08457135 Patent No. 5644031
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                                                                      TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TOPOLOGY: linear
ORIGINAL SOURCE:
STRAIN: Human Dlk
QUENCE 383 AA; 41201 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GNFELEILEISNTNSHLLNGYCCGMPAELRATKTIGCSPCTTAFRLCLKEYQTTEQGASI
                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/457,13
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                 APPLICATION NUMBER: 07/9
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                      FILING DATE: 01-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LABORDA, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                            STREET: 3000
STREET: Washington, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQ-CTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWPGTFSLIVEAWHDTNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STGCSFGNATTKILGGSSFVLSDP-----G-VGAIVLPFTERWTKSFTLILQA-LDMYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTCDLNYYGSGCAKFCR 198
                                                                                                                                                 NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,7 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LE TYPE: peptide
199 AA; 21952 MW; 208406 CN;
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ilarity 37.0%;
Conservative
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                                                  amino acid
                                                             383 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                             LABORDA,
                                                                                                                                                                                                                                                                                                                                                                                  Foley & Lardner
                                                                                                                                                                                                                                     01-JUN-1995
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   MW; 758273 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                      Jorge
Delta-Like Gene Expressed
                                                                                                                                                                                                                                                                                                                                                                                                                    Neuroendocrine Tumors
                                                                                                                                                                                                             07/989,537
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Pred. No. 1.84e-33;
51; Mismatches 66
                                                                                                                                                            29,768
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170 ESQYTSLEYDFRVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHI 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.5%; Score 95; DB 1; Length 385; Best Local Similarity 30.5%; Pred. No. 2.73e+00; Matches 18; Conservative 9; Mismatches 30; Indels
                                                                                                             Sequence 1, Application US/08597545
Patent No. 5580738
GENERAL INFORMATION:
APPLICANT: LABORDA, Jorge
TITLE OF INVENTION: Delta-Like Gene Expressed In
TITLE OF INVENTION: Neuroendocrine Tumors
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jorge
Delta-Like Gene Expressed In
Neuroendocrine Tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40399/166 NIHD
                                                                                                                                                                                                                                                                               E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,537
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: Mouse Dlk
ICE 385 AA; 41320 MW; 772804 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Patent No. 5644031
GENERAL INFORMATION:
APPLICANT: LABORDA, Jorge
TITLE OF INVENTION: Delta-Like Ger
TITLE OF INVENTION: Neuroendocrin
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 2007-5109
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 4039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5309
TELEFAX: (202)672-5399
                                                                         Sequence 1, Application US/08597545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08457135.
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TELEFAX: (202,)...
TELEEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRRACTERISTICS:
LENGTH: 385 amino acids
LENGTH: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                       Washington, D.C
                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                 ADDRESSEE:
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            Length 383;
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Best Local Similarity 32.6%; Pred. No. 1.11e+00;
Matches 14; Conservative 8; Mismatches 19; Indels
            Score 100; DB 1; Length 383
Pred. No. 1.11e+00;
8; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed In
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                                                                                              45 CQPGWQGPLCDQ-CVTSPGCL-HGLCGEPGQCICTDGWDGELC
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LABORDA, Jorge
APPLICANT: LABORDA, Jorge
TITLE OF INVENTION: Delta-Like Gene Expres
TITLE OF INVENTION: Neuroendocrine Tumors
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40399/166 NIHD
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,537
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN: Human Dlk
383 AA; 41201 MW; 758273 CN;
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REFERENCE/DOCKET NUMBER: 40399
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELERAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08597545 Patent No. 5580738
                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08597545.
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            Query Match 5.8%;
Best Local Similarity 32.6%;
Matches 14; Conservative
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STRAIN: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                 RESULT 6
ID US-08-597-545-2
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Best Local :
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                                                                                                                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9302147A.
                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9302147A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 ESQYTSLEYDFRVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 DPQYGFCEADNVCRCHVGWEGPLCDK-CVTAPGCV-NGVCKEPWQCICKDGWDGKFCEI 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 5.5%;
Local Similarity 30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 385 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
STRAIN: Mouse Dlk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/304/NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5399
TELEX: 404112
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                  APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/98
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                       STREET: FIVE FACCITY: PALO ALTO
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APPLICATION NUMBER:
                                                                                                             COUNTRY:
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                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 AA; 41320 MW; 772804 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 amino acids
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PCT/US93/02147A
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Pred. No. 2.73e+00;
9; Mismatches 3(
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                                                                                                                                                                                                                                                                                                                                                                                                        969 AA
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                             #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. GENERAL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08454455 Patent No. 5635601
                                                                                                                                                                                                                                                                                                               APPLICANT: Moyle, Matthew
APPLICANT: McLean, John W.
TITLE OF INVENTION: NOVEL BETA INTEGI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                        APPLICATION NUMBER: 08/193
FILING DATE: 09-FEB-194
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004
FILING DATE: 13-JAN-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670
                                                                                                                         PILING DATE: 30-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
08/193989
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 720 kb f:
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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FILING DATE:

14-MAR-1991

07/670607

08/004142

APPLICATION NUMBER: US/08/454,455

COUNTRY:

USA

94080

720 Kb floppy

INFORMATION:

NOVEL BETA INTEGRIN SUBUNIT

STANDARD;

PRT;

768

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Query Match
Best Local Similarity
Matches 17; Conser
                                                                                                                                         MOLECULE TYPE: protein SEQUENCE 969 AA; 106419 MW; 4660240 CN;
                                                                                                                                                                                                            TELEPHONE: (415) 494-7622
TELEFAX: (415) 857-063
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acids
184 CDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCH
                             733 CPLGYFGDTAARRCR-RCHK-GCETCSSRAATQCLSCRRGFYHH 774
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 09-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          NAME: NEELEY PH.D., RICHARD L
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                               5.4%;
ilarity 38.6%;
Conservative
                                                                                                                                                                                               amino acid
                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19930309
                                                                                                                                                                                                                                                                                                                                                                                                                                      US 07/848,629
                                                                 Score 94; DB 2; 1
Pred. No. 3.26e+00;
6; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                CHIR-009/00US
                                                                      19;
                                                                                                      Length 969
227
                                                                      Indels
                                                                    <u>ب</u>
                                                                    Gaps
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38 NSFQGTFVYERNGSFS-THEIWHRVESDGAVR-ERLL 72
                                                                                                                                                                                                                           Sequence 18, Application US/08260202A.
                                                                                                           205 GHSTCSETGEIICLTGWQGDYCHIP 229
                                                                                               563 GHGEC-EAGRCQCFSGWEGDRCQCP 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMONICATION INFORMATION
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO. 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 316 amino acids
TYPE: amino acid
 LENGTH: 769 amino acids TYPE: Amino Acid
                                                    Query Match 5.3%;
Best Local Similarity 48.0%;
Matches 12; Conservative
                      TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                   Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                    JT 12
US-08-260-202A-18
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                                                                                                                                      Query Match 5.3%; Score 92; DB 1; Length 768; Best Local Similarity 48.0%; Pred. No. 4.65e+00; Matches 12; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08454455
Patent No. 5635601
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Moyle, Matthew
APPLICANT: McLean, John W.
TITLE OF INVENTION: NOVEL BETA INTEGRIN SUBUNIT
UNDBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                  769 AA
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P0699C2D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 768 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPENATING SISTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA: US/08/454,455
APPLICATION NUMBER: US/08/454,455
FILING DATE: 30-May-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/193989
FILING DATE: 09-FEB-1994
PRIOR APPLICATION NUMBER: 08/004142
FILING DATE: 13-JAN-1993
PRIOR APPLICATION NUMBER: 08/004142
FILING DATE: 13-JAN-1993
APPLICATION NUMBER: 07/670607
FILING DATE: 14-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P0699C2D2
                                                                                                      TOPOLOGY: Linear
NCE 768 AA; 84405 MW; 2945477 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Generated, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08454455.
                                                                                                                                                                                  563 GHGEC-EAGRCQCFSGWEGDRCQCP 586
                                                                                                                                                                                              205 GHSTCSETGEIICLTGWQGDXCHIP 229
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                  STANDARD;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
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US-08-454-455-6
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Sequence 18, Application US/08260202A
Patent No. 5573910
GENERAL INFORMATION:
APPLICANT: Deretic, Vojo
APPLICANT: Martin, Daniel W.
TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN
TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIEN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
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                                           Score 92; DB 1; Length 769;
Pred. No. 4.65e+00;
6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: TX
COUNTRY: USA
ZUNTTY: USA
ZUNTTR: TX
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,202A
                                                                                                                                                                                                                                                                                              316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,202
FILING DATE: 15-UN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/017,114
FILING DATE: 12-FEB-1993
ATTONNEY/AGGNT INFORMATION:
NAME: HOGGINS, DATIel S.
REGISTRATION NUMBER: 31,0256
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
769 AA; 85631 MW; 2953052 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
WCE 316 AA; 34564 MW; 500303 CN;
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ID PC
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Best Local S
Matches 1
          US-08-017-114-18
                                                                                                                                       SEQUENCE
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                                                    112 NPIQFPFSFSWPGTFSLIVEAWHDTNNSGNARTNKLL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application GENERAL INFORMATION:
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112 NPIQFPFSFSWPGTFSLIVEAWHDTNNSGNARTNKLL
                                                                                            y Match 5.1%;
Local Similarity 35.1%;
hes 13; Conservative
                                                              38 NSFQGTFVYERNGSFS-THEIWHRVESDGAVR-ERLL 72
                                                                                                                                                                                                              TELEFAX: 713/789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: POSTAL COD
APPLICANT: TELEPHONE I
APPLICANT: TELEPAX:
TITLE OF INVENTION: DI
TITLE OF INVENTION: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/017,114
FILING DATE: 12 February 1993 (12.02.93)
ATTORNEY/AGENT INFORMATION:
NAME: HODGINS, DANIEL S.
REGISTRATION NUMBER: 31,026
                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94
FILING DATE: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: UT TELECOMMUNICATION INFORMATION: TELEPHONE: 512/320-7200
                                                                                                                                      MOLECULE TYPE: peptide
ENCE 316 AA; 34572 MW; 501312 CN;
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                         TELEPHONE: 514/1-
TELEPHONE: 514/1-
THI TEAX: 713/789-2679
                                                                                                                                                           STRANDEDNESS: Sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
                                                                                                                                                                             LENGTH: 316 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                              77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POSTAL CODE: 78701
TELEPHONE NO: (512)499-4462
TELEFAX: (512)499-4523
TELEFAX: (512)499-4523
VENTION: DETECTION OF CONVERSION TO MUCOIDY IN PSEUDOMONAS VENTION: AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                         FLOPPY DISK
                                                                                                                                                                     single
          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Austin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 West 7th Street
                                                                                                                                                                                                                                                                                                                                                               PCT/US94/02034
                                                                                           Score 88; DB 2; I
Pred. No. 9.36e+00;
9; Mismatches 13
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          PRT;
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                              APPLICANT:
         APPLICANT: APPLICANT:
  FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
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Query Match 5.1%;
Best Local Similarity 35.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: N/A
INFORMATION FOR SEQ ID NO: 18.
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                              Sequence 4, Application US/08447554.
                                                      Sequence 4, Application US/08447554 Patent No. 5661003 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08017114
                                                                                                                                                                                                                                                        112 NPIQFPFSFSWPGTFSLIVEAWHDTNNSGNARTNKLL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Deretic, Vojo

APPLICANT: Martin, Daniel W.

TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCCOLDY IN

TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIEN

TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIEN
                                                                                                                                                                                                                                                                       38 NSFQGTFVYERNGSFS-THEIWHRVESDGAVR-ERLL 72
                                                                                                                                                                                                                                                                                                                                                       STRANGEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
MOLECULE TYPE: peptide
UENCE 316 AA; 34572 MW; 501312 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UTSK:205/HOD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/320-7200
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US
FILING DATE: 19930212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Texas
7: USA
FUSHIMI, KIYOHIDE
UCHIDA, SHINICHI
SASAKI, SEI
MARUMO, FUMIAKI
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                  STANDARD;
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FUMIAKI WATER CHANNEL

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CC CONTENT NOTES B
COUNTRY: USA
CC CONTENT BEALDRESS:
CC CONTENT: 2000 Pennsylvania Ave. NW, Ste. 5500
CITY: Washington, DC
CC CITY: Washington, DC
CC CONTENT: USA
CC CONTENT
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Search completed: Fri Jun 12 12:06:51 1998 Job time: 8 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Fri Jun 12 12:03:56 1998; MasPar time 10.84 Seconds 775.242 Million cell updates/sec

>US-08-083-590A-2 (1-230) from US08083590A.pep (2 of 2) 1734

Scoring table:

Description: Perfect Score: Sequence: PAM 150 Gap 11 1 MHWIKCLLTAFICFTVIVQV.....ETGEIICLTGWQGDYCHIPK 230

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 42.868; Variance 79.045; scale 0.542

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 222229871654 32222987654 32222987654 | Result |
|---|----------------|
| 1734 1728 17228 775 735 7480 480 480 480 480 103 1103 1103 1103 1103 1103 1103 110 | Score |
| 202448990 2024487 2022490 2024490 202490 2 | Query Match |
| 833 830 728 728 1120 11404 1404 1402 259 259 259 271 383 383 383 383 383 385 385 385 385 385 | Length |
| | DB |
| A312087 A31204 S00670 S00670 I180719 I180719 A36666 A36666 S14648 S42367 S44749 S44749 S53718 S53718 S53718 S54753 | ID |
| gene Delta protein pr neurogenic protein pr gene Delta protein pr C-Delta-1 · chicken DELTA-like 1 · mouse Jagged protein precur gene serrate protein precu gene serrate protein can lag-2 protein · Caeno delta-like dlk homeot integrin beta-3 subun fetal antigen 1 · hume fetal antigen 1 · hum fetal antigen 2 · chic fetal antigen 3 · chic fetal antigen 2 · | Description |
| 0.00e+00 0.00e+00 0.00e+00 0.00e+00 3.57e-141 1.35e-131 2.06e-95 2.63e-76 2.63e-76 7.32e-07 3.29e-02 8.83e-02 8.83e-02 8.83e-02 8.83e-02 6.37e-02 6.37e-02 6.37e-01 1.33e-01 1.39e-01 3.20e-01 3.20e-01 3.20e-01 | Pred. No. |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | .27 | 26 | 25 | 24 |
|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------------|-----------------------|-----------------------|----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|
| 87 | 87 | 87 | 87 | 87 | 88 | 88 | 89 | 88 | 88 | 90 | 90 | 91 | 91 | 91 | 90 | 92 | 92 | 92 | 94 | 94 | 94 |
| 5.0 | 5.0 | 5.0 | 0 | 5.0 | 5.1 | 5. L | 5. 1- | 5.1 | 5.1 | 5.2 | 5.2 | 5.2 | 5.2 | 5.2 | 5.2 | 5. ω | 5. ω | 5.3 | 5. 4. | 5.4 | 5.4 |
| 2515 | 1928 | 788 | 271 | 92 | 782 | 715 | 408 | 316 | 47 | 1820 | 937 | 885 | 858 | 858 | 522 | 769 | 768 | 590 | 1203 | 975 | 969 |
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| S47008 | JS0610 | A26547 | JT0750 | D37057 | A61625 | S76492 | B64708 | A47064 | S11530 | A55494 | 153282 | JC4732 | 1QBB | 1QBA | JT0980 | A41029 | B41029 | QRBYPR | A49175 | JC5570 | A39490 |
| tenascin-like protein | beta-galactosidase (E | platelet glycoprotein | water channel protein | epithelial cell glyco | tenascin-like protein | hypothetical protein | glutamate permease - | algN protein - Pseudo | purothionin gamma - p | latent transforming g | gene PACE4 protein - | beta-N-Acetylhexosami | chitobiase (EC 3.2.1. | chitobiase n-acetyl-b | cytochrome P450 52A2, | integrin beta-8 chain | integrin beta-8 chain | arginine transport pr | Motch B protein - mou | subtilisin-like prote | serine proteinase (EC |
| 5.07e+00 | 5.07e+00 | 5.07e+00 | 5.07e+00 | 5.07e+00 | 3.77e+00 | 3.77e+00 | 2.79e+00 | 3.77e+00 | 3.77e+00 | 2.06e+00 | 2.06e+00 | 1.52e+00 | 1.52e+00 | 1.52e+00 | 2.06e+00 | 1.12e+00 | 1.12e+00 | 1.12e+00 | 6.01e-0 | 6.01e-01 | 6.01e-0 |

ALIGNMENTS

| #formal_name Drosophila melanogaster | ORGANISM |
|--|---|
| A31246 #type complete neurogenic protein Delta precursor - fruit fly (Drosophila | RESULT ENTRY TITLE |
| RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPK 230 | Db 181 Qy 181 |
| SWPGTFSLIVEAWHDTNNSGNATNKLLIQRLLVQQVLEVSSEWK!NKSESQYTSLEXDF 180 | 0b 121 Qy 121 |
| CKTRFRVCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPESF 120 | Db 61 Qy 61 |
| MHWIKCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGS 60 | рь 1 Qy 1 |
| <pre>/ Match 100.0%; Score 1734; DB 2; Length 833; Local Similarity 100.0%; Pred. No. 0.00e+00; les 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre> | Query Match Best Local Matches 2 |
| CS ne FlyBase:Dl ##cross-references FlyBase:FBgn0000463 # #length 833 #molecular-weight 88812 #checksum 2566 | GENETICS #gene ##c ##c |
| ##Status Pretiminary ##molecule_type mRNA ##residues 1-833 ##label MUS ##cross-references EMBL:Y00222 | # # # # # |
| S1908 S1908 Sion Submi | REFERENCE #authors #submission #accession |
| 20# | ORGANISM DATE |
| 1 S19087 #type complete gene Delta protein precursor - fruit fly (Drosophila melanogaster) | RESULT ENTRY TITLE |

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                                                          #authors Kopczynski, C.C.; Alton, A.K.; Fechtel, K.; Kooh, P.J.;
Muskavitch, M.A.T.
#journal Genes Dev. (1988) 2.1723-1735
#title complex and encodes a protein related to blood coagulation factors and encodes a protein related to blood coagulation factors and epidermal growth factor of vertebrates.
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EMBO J. (1987) 6:3431-3440
The neurogenic gene Delta of Drosophila melanogaster is
expressed in neurogenic territories and encodes a putative
transmembrane protein with EGF-like repeats.
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31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
16-Feb-1997
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melanogaster)
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99.6%; Pred. No. 0.00e+00;
' Wismatches 0;
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Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Jish Horowicz, D. Nature (1995) 375:787-790 Expression of a Delta homologue in prospective neurons in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Gallus gallus #common_name chicken
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
13-Sep-1996
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##cross-references EMBL:U26590; NID:9882411; PID:9882412
.X #length 728 #molecular-weight 79861 #checksum 1765
                                                                                                                                                                                                                                                                                                  181 RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPK 230
                                                                                                                                                                                                                                                                             181 RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPK 230
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##molecule_type mRNA
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Bettenhausen, B.; de Angelis, M.H.;
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#accession I48324
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                                                                                                                                                                                                                                                  7
                                                                                      CDDHYYGFGCNKFCRPRDDFFGHYACDQNGNKTCMEGWMGPECN 231
                                                                                                                                                                                                       YFKVCLKEYQSRVTAGGPCSFGSGSTPVIGGNTFNLKAS-RGNDR---NRIVLPFSFAWP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDP 223
                                                                         CDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCH
                                                                                                                                GTFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVT
                                                                                                                                                                                         RFRYCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWP
                                                                                                                                                                                                                                                  LLTAFICFTVIVQVH-SSGSFELRLKYFSNDHGRDNEGRCCSGESDGATG-KCL-GSCKT 63
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                                                                                                                                                           RSYTLLYEAW-DSSND-TIQPDSI-IEKASHSGMINPSRQWQTLKQNTGIAHFEYQIRVT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTCDLNYYGSGC
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                                                                                                                                                                                                                                                                                                        32.8%;
Similarity 37.9%;
85; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                      Lindsell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, Cell (1995) 80:909-917
Jagged: a mammalian ligand that activates Notchl. A56136
              A36666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jagged protein precursor - rat
#formal_name Rattus norvegicus #common_name Norway rat
28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change
  serrate
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#type complete
tein precursor
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Pred. No. 2.06e-95;
52; Mismatches 76;
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Pred. No. 1.35e-131;
38; Mismatches 68;
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fruit fly (Drosophila
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#accession S16878
    ##molecule_type mRNA
    ##residues 1-1351,'T',1353-1408 ##label THO2
###cross-references EMBL:X56811
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#accession S16148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references FlyBase:FBgn0004197
RDS transmembrane protein
RY #length 1404 #molecular-weight 150245 #checksum
                                                                                                                                                              ##residues 1-1408 ##label THO1
##cross-references EMBL:X56811
                                                                                                                                                                                                       ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 TAFRLCLKEYQTTEQGASISTGCSFGNATTKILGGSSFVLSDP------G-VGAIVLPFT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
##residues 1-1404 ##label
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Local Similarity 36.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRYTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRERVCLKHYQATID-TT-SQ-CTYGDVITPILGENSVNLTDAQREQNKGFTNPIQEPES 119
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                                                                    Thomas, U. submitted to S16878
                                                                                                                                           S16878
                                                                                                                                                                                                                                                                                                 Thomas, U.; Speicher, S.A.; Knust, E
Development (1991) 111:749-761
The Drosophila gene Serrate encodes
protein with a complex expression
                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Drosophila melanogaster
31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change
16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes Dev. (1990) 4:2188-2201
The gene Serrate encodes a putative EGF-like transmembrane protein essential for proper ectodermal development in Drosophila melanogaster.

10:25 MJID:91099666
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#formal_name Drosophila melanogaster
19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change
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Pred. No. 2.63e-76;
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Nature (1994) 368:150-154
Sequence of C. elegans lag-2 reveals a cell-signalling domain shared with Delta and Serrate of Drosophila.
                                                                    #domain signal sequence #status predicted #label SIG\
#product gene serrate protein #status predicted #label
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Exp homology *label EG01\
Exp homology *label EG02\
Exp homology *label EG02\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 TAFRLCLKEYQTTEQGASISTGCSFGNATTKILGGSSFVLSDP-----G-VGAIVLPFT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 FRWTKSFTLILQA-LDMYNTSYPDAERLIEETSYSGVILP-SPEWKTLDHIGRNARITYR 236
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#length 402 #molecular-weight 44603 #checksum 6894
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#length 1408 #molecular-weight 150645 #checksum
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Pred. No. 2.63e-76;
59; Mismatches 70; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homology #label EG14\
#superfamily EGF homology glycoprotein; transmembrane protein
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#domain transmembrane #status
#domain intracellular #status
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Conservative 5
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412,452,558,739,
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Ransom, D.G.; Hens, M.D.; DeSimone, D.W.
Dev. Biol. (1993) 160:265-275
Integrin expression in early amphibian embryos: CDNA cloning
and characterization of Xenopus beta 1, beta 2, beta 3, and
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integrin beta-3 subunit - African clawed frog
14 formal_name Xenopus laevis #common_name African clawed frog
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Laborda, J.; Sausville, E.A.; Hoffman, T.; Notario, V.
#journal J. Biol. Chem. (1993) 268:3817-3820
#title aptetive mammalian homeotic gene differentially expressed in small cell lung carcinoma and neuroendocrine
#cross-references MUID:93179372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-383 ##label LAB
##cross-references EMBL:Z12172; NID:g38478; PID:g38479
##note extracted from NCBI backbone (NCBIP:125735)
##note species designations for this sequence report and for
A45484 originally were transposed in NCBI backbone
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Length 402
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Pred. No. 2.36e-02;
8; Mismatches 19; Indels
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                                                                                                              122 VTCARNYFGNRCENFCDAHLAKAARKRCDAMGRLRCDIGWMGPHC 166
                                                                                                                                          184 CDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYC 226
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*length 788  #molecular-weight 87490
  Score 133; DB 2; Le
Pred. No. 7.32e-07;
8; Mismatches 21;
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Pred. No. 3.29e-02;
7; Mismatches 12;
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#cross-references MUID:94040374
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Best Local Similarity 32.6%;
Matches 14; Conservative
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Best Local Similarity 39.5%;
Matches 15; Conservative
  Query Match 7.7%;
Best Local Similarity 35.6%;
Matches 16; Conservative
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184 CDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYC
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##residues 1-259 ##label JEN
#XY #length 259 #molecular-weight 27316 #checksum
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                                                Lee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J. Biochim. Biophys. Acta (1995) 1261:223-232 dlk, pG2 and Pref-1 mRNAs encode similar proteins belonging to the EGF-like superfamily. Identification of polymorphic
                                                                                                                                                                           #formal_name Homo sapiens #common_name man
06-pec-1996 #sequence_revision 06-pec-1996 #text_change
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Primary structure of human fetal antigen 1 (FA1), a putative
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fetal antigen 1 homeotic protein - human
#formal_name Homo sapiens #common_name man
03-Feb-1994 #sequence_revision 03-Feb-1994
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K.; Larsson, L.I.; Enghild, J.J.; Teisner, B.
Eur. J. Biochem. (1994) 225:83-92
Protein structure of fetal antigen 1 (FAI). A novel
circulating human epidermal-growth-factor-like protein
expressed in neuroendocrine tumors and its relation to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
                                                                                                                                                                                                                                                                                                                                                                                                  ##status preliminary
##molecule_type mRNA
##residues 1-788 ##label SHE
##cross-references GB:M35198; GB:J05522; NID:g186506; PID:g186507
##cross-references GB:M35198; AB:J05522; NID:g186506; PID:g186507
##cross-references GB:M35198; AB:J05522; NID:g186506; PID:g186506; PID:g186506; PID:g186506; PID:g186506; PID:g186506; PID:g186
                                                                                                                                      193
                                                                                                                                                                                                    539 CDNFSCVRHKGLLCGGNGDC-DCGECVCRSGWTGEYCN 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 CDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
##residues 1-344,346-383 ##label LAB
##cross-references EMBL:U15979; NID:g562105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type mRNA
#residues 1-228,302-383 ##label LEW
##coss-references EMBL:U15981; NID:g562109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-383 ##label |
##cross-references EMBL:U15979
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                                                                                                                                   CAKF-C-RPRDD-SFGHSTCSETGEIICLTGWQGDYCH
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                                                                                                                                                                                                                                                                  h 5.8%;
Similarity 36.8%;
14; Conservative
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Similarity 32.6%;
14; Conservative
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Complete amino acid sequence of a novel integri (beta6) identified in epithelial cells using chain reaction.

Complex MID:90307659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A37057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sheppard, D.; Rozzo, C.; Starr, L.; Pytela, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A37057 #type complete
integrin beta-6 chain - human
#formal_name Homo sapiens #common_name man
15-Feb-1991 #sequence_revision 13-Sep-1991 #text_change
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predicted #label MAT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *product homeotic protein dlk long form *status
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Pred. No. 6.37e-02;
9; Mismatches 11
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Pred. No. 8.83e-02;
8; Mismatches 19;
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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Fri Jun 12 12:04:53 1998; MasPar time 7.25 Seconds 795.610 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US-08-083-590A-2 (1-230) from US08083590A.pep (2 of 2) 1734 1 MHWIKCLLTAFICFTVIVQV......ETGEIICLTGWQGDYCHIPK 230

Scoring table: : PAM 150 Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 44.483; Variance 66.618; scale 0.668

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 222118 2322118 2322118 | Result No. |
|---|-----------------------|
| 1722 732 732 732 113 110 100 101 100 101 100 97 97 97 97 99 99 99 99 99 99 99 | Score |
| 02442 03442 03442 03442 03443 03443 03443 03443 03443 03443 0343 03443 0343 | Query Match Length |
| 71408 1408 1408 5152 516 517 517 517 517 318 318 318 318 318 318 318 318 318 318 | |
| مر مر مر مر م _ن مر | DB |
| DL_DROME DLL1_RAT DLL1_RAT SERR_DROME LAG2_CAEEL APX1_CAEEL DLK_HUMAN CDA2*YEAST 1TB6_CAVPO LML2_CAEEL DLX_MOUSE YLZ5_CAEEL PAC4_HUMAN CAN1_YEAST 1TB8_RABIT 1TB8_RABIT 1TB8_RACIT PAC4_RAT LAG5_MOUSE DYHC_PARTE DYHC_PARTE DYHC_PARTE THG2_WHEAT THG2_WHEAT | ID |
| NEUROGENIC LOCUS DELTA DELTA-LIKE PROTEIN 1 PETTA-LIKE PROTEIN 1 PETTA-LIKE PROTEIN PRECURS ANC-1 PROTEIN PRECURS OADX-1 PROTEIN PRECURS OADX-1 PROTEIN PRECURS OELTA-LIKE PROTEIN PRE CHITIN DEACETYLASE 2 PINTEGRIN BETA-6 SUBUNI LAMININ-LIKE PROTEIN K DELTA-LIKE PROTEIN K DELTA-LIKE PROTEIN PRE HYPOTHETICAL 89.2 KD SUBTILISIN-LIKE PROTEA ARGININE PETA-8 SUBUNI INTEGRIN BETA-8 SUBUNI INTEGRIN BETA-8 SUBUNI CYTOCHROME P450 LIIA2 SUBTILISIN-LIKE PROTEA LAMININ ALPHA-5 CHAIN DYNEIN HEAVY CHAIN, CY GAMMA-2 PUROTHONIN. | Description |
| 1.000+00 1.00+100 1.25e-161 1.25e-93 1.28e-05 8.66e-03 8.66e-03 8.7e-03 2.74e-02 2.74e-02 2.74e-02 8.43e-02 8.43e-02 8.43e-01 1.76e-01 | Pred. No. |

| 4.4 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 5 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 |
|-----------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-----------------------|------------------------|
| 8 0 | 83 | 83 | 83 | 83 | 83 | 84 | 84 | 83 | 83 | 84 | 85 | 8 5 | 85 | 86 | 87 | 86 | 87 | 87 | 87 | 88 |
| 4.4 | . 80 | 4.8 | 8 | 4.8 | 4.8 | 4.8 | 4.8 | 8 | 4.8 | 4.8 | 4.9 | 4.9 | 4.9 | 5.0 | 5.0 | 5.0 | | | 5.0 | 5.1 |
| 2415 | 1124 | 873 | 811 | 637 | 456 | 433 | 396 | 328 | 284 | 87 | 3649 | 672 | 543 | 1808 | 1295 | 858 | 788 | 298 | 271 | 316 |
| - | μ. | _ | _ | 1 | <u> </u> | _ | H | ۳ | 4 | ₩ | ۳, | μ. | ۴ | ۳ | ا | ۳ | j- -3 | μ, | ۳ | سر |
| PGCA_HUMAN | TIE2_HUMAN | FS21_DROME | FS22_DROME | YAO7_SCHPO | YDE8_SCHPO | YBL4_YEAST | DUT_VZVD | CHIT_PHAVU | YKGD_ECOLI | YI74_BURCE | ACVS_NOCLA | YCDR_ECOLI | FAT2_YEAST | TENA_CHICK | GLP1_CAEEL | CYAG_DICDI | ITB3_HUMAN | YAKI_YEAST | AQP2_RAT | MUCB_PSEAE |
| AGGRECAN CORE PROTEIN | ANGIOPOIETIN 1 RECEPTO | FASCICLIN II, MEMBRANE | FASCICLIN II, PHOSPHAT | PUTATIVE 73.4 KD TRANS | HYPOTHETICAL 52.4 KD P | HYPOTHETICAL 50.8 KD P | DEOXYURIDINE 5'-TRIPHO | ENDOCHITINASE PRECURSO | HYPOTHETICAL TRANSCRIP | INSERTION ELEMENT IS40 | DELTA-(L-ALPHA-AMINOAD | HYPOTHETICAL 77.4 KD L | PEROXISOMAL-COENZYME A | TENASCIN PRECURSOR (TN | GLP-1 PROTEIN PRECURSO | ADENYLATE CYCLASE, GER | PLATELET MEMBRANE GLYC | HYPOTHETICAL 35.1 KD P | AQUAPORIN-CD (AQP-CD) | SIGMA FACTOR ALGU REGU |
| 4.08e+00 | 4.08e+00 | 4.08e+00 | 4.08e+00 | 4.08e+00 | 4.08e+00 | 2.91e+00 | 2.91e+00 | 4.08e+00 | 4.08e+00 | 2.91e+00 | 2.08e+00 | 2.08e+00 | 2.08e+00 | 1.47e+00 | 1.04e+00 | 1.47e+00 . | 1.04e+00 | 1.04e+00 | 1.04e+00 | 7.35e-01 |

ALIGNMENTS

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REQUENCE FROM N.A.

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                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
DELTA-LIKE PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
5A647702 CRC32;
                                       01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DELTA-LIKE PROTEIN 1 PRECURSOR (DELTA1).
             722 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
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SIMILARITY
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EGF-LIKE 3.
EGF-LIKE 4, C
EGF-LIKE 5.
EGF-LIKE 7, C
EGF-LIKE 7, C
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              PRT;
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78448
              STANDARD;
                                                                                                            MUS MUSCULUS (MOUSE)
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476
722 AA;
             DLL1_MOUSE
Q61483;
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MHWIKCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGAFGKCLGS 60
                                                                                                                                                                                                     , CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MHWINCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLGS 60
                                                                                                                                                                                , CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                        DELTA PROTEIN.
EXTRACELLULAR (POTENTIAL)
                                                                                   CYTOPLASMIC (POTENTIAL).
NEUROGENESIS; REPEAT; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GK -> ET (IN REF. 2).

G -> A (IN REF. 2).

S -> T (IN REF. 2).

E967E662 CRC32;
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                                                                                                                                                                                                                                                     SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
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SIMILARITY.
                                                                                                                         EGF-LIKE 3.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 7, CR
EGF-LIKE 9, CR
EGF-LIKE 9, CR
EGF-LIKE 9, CR
EGF-LIKE 18, SIMILARITY.
EN SIMILARITY.
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SIMILARITY.
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                                                                                                EGF-LIKE 1.
EGF-LIKE 2.
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POTENTIAL.
POTENTIAL.
POTENTIAL.
GK -> ET (1
                                                                    POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     larity 99.1%;
Conservative
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nes 228; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            880 AA;
DIFFERENTIATION;
EGF-LIKE DOMAIN;
                                          CHAIN
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PROSITE; PS001022; EGF_1; 8.
PROSITE; PS01186; EGF_2; 8.
PROSITE; PS01187; EGF_CA; 2.
SIGNAL; EGF-LIKE DOMAIN; GLYCOPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISTBIO G., HEBSHI L., BOULTER J., WEINMASTER G.;
SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: MAY BE INVOLVED IN CELL-TO-CELL COMMUNICATION IN
MAMMALIAN EMBRYOS. MAY HAVE A ROLE IN CELLULAR INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RATTUS NORVEGICUS (
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
SIMILARITY: TO DROSOPHILA DELTA PROTEIN.
L; U78889; G1699046; -.
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(REL. 35,
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               CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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ANNOTATION UPDATE)
POTENTIAL.

DELTA-LIKE PROTEIN 1.

EXTRACELULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 5.

EGF-LIKE 5.

EGF-LIKE 6.

EGF-LIKE 7.

EGF-LIKE 8.

EGF-LIKE 10.

EGF-LIK
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No. 1.85e-161;
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Query Match
Best Local S
Matches 10
C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
C -!- TISSUE SPECIFICITY: APPEARS TO BE RESTRICTED EXCLUSIVELY I CELLS OF ECTODERMAL ORIGIN.
C -!- SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO THE INNER OF EMBRYO IS ONE OF THE FIRST STEPS OF CNS DEVELOPMENT IN THIS PROCESS IS UNDER CONTROL OF THE NEUROGENIC GENES.
-!- NOTCH AND SERRATE MAY INTERACT AT THE PROTEIN LEVEL, IT IS CONCELVABLE THAT THE SERRATE AND DELTA PROTEINS MAY COMPET FOR BINDING WITH THE NOTCH PROTEIN.
-!- SIMILARITY: CONTAINS 14 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                        SEQUENCE
MEDLINE;
FLEMING R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                 FLEMING R.J., SCOTTGALE T.N., DIEDERICH R.J., ARTAVANIS-TSAKONAS GENES DEV. 4:2188-2201(1990)
-I- FUNCTION: ESSENTIAL FOR PROPER ECTODERMAL DEVELOPMENT. SERRAT MAY REPRESENT AN ELEMENT IN A NETWORK OF INTERACTING MOLECULE OPERATING AT THE CELL SURFACE DURING THE DIFFERENTIATION OF
                                                                                                                                                                                                                                                                            MEDLINE; 91347903.
THOMAS U., SPEICHER S.A., KNUST
DEVELOPMENT 111:749-761(1991).
                                                                                                                                                                                                                                                                                                                                                             DROSOPHILA MELANOGASTER (FRUIT FLY)
EUKARYOTA; METAZOA; ARTHROPODA; INS
                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                              P18168;
01-NOV-1990
                                                                                                                                                                                                                                                                                                                       STRAIN-OREGON-R;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         SER OR BD
                                                                                                                                                                                                                                                                                                                                                                                                       SERRATE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 ALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGS-GPP--C--ACRTFFRVCLKHYQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDEHYYGEGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -DINNSGNARINKLLIQRILLVQQVLEVSSEWKINKSESQYTSLEYDFRVTCDLNYYGSGC
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larity 47.7%;
Conservative
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26, LAST SEQUENCE UPDATE)
33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                      (BEADED
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Pred.
38; M
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                                                                                                                         MEMBRANE PROTEIN.
NO BE RESTRICTED EXCLUSIVELY
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No. 8.02e-160;
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    LOCUS DELTA PROTEIN
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NT IN I
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Gaps 11;
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IN NATURE 368:150-154(1994).

C. -!- FUNCTION: PUTATIVE INTERCELLULAR SIGNAL FOR LIN-12 AND GLP-1

ERCEPTORS.

C. -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. -!- SIMILARITY: CONTAINS 1 DSL (DELTA/SERRATE/LAG-2 DOMAIN), WHICH IS CONTAINS 1 DSL (DELTA/SERRATE/LAG-2 DOMAIN), WHICH IS CONTAINED TO BIND NOTCH IN DELTA AND SERRATE.

C. -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

EMBL; X77495; G459579; -.-

RR PROSITE; PS001186; EGF-1; 2.

RR PROSITE; PS01186; EGF-2; 2.

RR DIFFERENTIATION; REPEAT; TRANSMEMBRANE; EGF-LIKE DOMAIN;

GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IS
                                                                                                                                                                                                                                                                                                                                                                                                                            67 CNLIALI-LILLVHKISAAGNFELEILEISNTNSHLLNGYCCGMPAELRATKTIGCSPCT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAENORHABDITIS ELEGANS.
EURARYOTA: METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 FRWTKSFTLILQA-LDMYNTSYPDAERLIEETSYSGVILP-SPEWKTLDHIGRNARITYR
                                                                                                                                                                                                                                                                                                                                             Score 480; DB 1; Length 1408;
Pred. No. 1.25e-93;
59; Mismatches 70; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 FRVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 VRVQCAVTYYNTTCTTFCRPRDDQFGHYACGSEGQKLCLNGWQGVNC 283
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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POTENTIAL.

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LAG2_CAEEL STANDARD; PRT; 402 AA. P45442; REL. 32, CREATED)
01-NOY-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOY-1997 (REL. 35, LAST SEQUENCE UPDATE)
101-NOY-1997 (REL. 35, LAST ANNOTATION UPDATE)
1046-2 PROTEIN PRECURSOR.
106-2 OR LET-461.
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EGF-LIKE 1.
EGF-LIKE 2.
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Best Local Similarity 36.1%;
Matches 82; Conservative
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STRAIN-BRISTOL N2;
MEDLINE; 94187845.
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EGF-LIKE 1.

EGF-LIKE 4.

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EGF-LIKE 4.

EGF-LIKE 7.

EGF-LIKE 6.

EGF-LIKE 7.

EGF-LIKE 9.

EGF-LIKE 9.

EGF-LIKE 9.

EGF-LIKE 10.

EGF-LIKE 10.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 12.

EGF-LIKE 13.

EGF-LIKE 13.

EGF-LIKE 13.

EGF-LIKE 14.

EGF-LIKE 13.

EGF-LIKE 13.

EGF-LIKE 14.

EGF-LIKE 14.

EGF-LIKE 17.

EGF-LIKE 18.

EGF-LIKE 18.

EGF-LIKE 19.

EG
  EMBL; X56811; G8564; -.
EMBL; M35759; G158606; -.
PIR, A36666; A3666.

PIR, A36666; A36878

PIRS, S16878

PIRSP; P00743; 1APO.

PIRSASE; FB90004197; Ser.

PROSITE; PS001010; ASX_HYDROXYL; 7.

PROSITE; PS01186; EGF_1; 14.

PROSITE; PS01187; EGF_CA; 5.

PROSITE; PS01187; EGF_CA; 5.
                                                                                                                                                                                                                                                                  SERRATE PROTEIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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1408
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P41990;
01-NOV-1995
                           DOMAIN
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00022; EGF_1; PROSITE; PS01186; EGF_2; DIFFERENTIATION; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MELLO C.C., DRAPER B.W., CELL 77:95-106(1994).
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MEDLINE; 94208066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
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EUKARYOTA; METAZOA; ACC
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01-NOV-1995 (REL. 32,
01-FEB-1996 (REL. 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
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ABP FATE. CONTRIBUTES TO THE ESTABLISHMENT OF THE DORSAL-VENTRAL
AXIS IN THE EARLY C.ELEGANS EMBRYO.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 4 COMPLETE AND 1 INCOMPLETE EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%;
35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183
204
215
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245
254
254
265
105
105
     55818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACOELOMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST
LAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIESS J.R.;
     WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Œ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                   APX-1 PROTEIN.

EXTRACELLULAR (POTENTIAL)
POTENTIAL.

CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 133; DB 1;
Pred. No. 7.12e-09;
                                                EGF-LIKE 4
EGF-LIKE 5
EGF-LIKE 5
EGF-LIKE 5
EGF-LIKE 5
EGF-LIKE 6

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARI
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
G->D: IN S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,;
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                 Y SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y SIMILARITY.
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                                                                                                                                                                                                                                                                                                                        SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 515
                                                                                                                                                                                                                                                                                                                                                                          ۰. T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SA37; SUPPRESSES LIN-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                          (INCOMPLETE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECERNENTEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHABDITIDA.
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Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLK_HUMAN STANI
P80370;
01-NOV-1995 (REL. 3:
01-FEB-1996 (REL. 3:
01-NOV-1997 (REL. 3:
DELTA-LIKE PROTEIN I
             PEPTIDE
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: FAI IS FOUND WITHIN THE STROMAL CELLS IN CLOSE CONTACT TO THE VASCULAR STRUCTURE OF PLACENTAL VILLI, YOLK SAC, FETAL LIVER, ADRENAL CORTEX AND PANCREAS AND IN THE BETA CELLS OF THE ISLETS OF LANGERHANS IN THE ADULT PANCREAS. FOUND ALSO IN SOME FORMS OF NEUROBODCRINE LUNG TUMOR TISSUE.
-!- PTM: N- AND O-GLYCOSYLATED.
-!- ALTERNATIVE PRODUCTS: AT LEAST ONE SHORTER PROTEIN IS DERIVED FROM THE SAME GENE BY ALTERNATIVE SPLICING.
-!- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
EMBL; U15979; G562106; -.
EMBL; U15981; G562106; -.
EMBL; U15981; G562107.
                                                                                                                        SIGNAL
                                                                                                                                                                                           PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JENSEN C.H., TEISNER B., HOJRUP P., RASMUSSEN H.
NIELSEN B., SKJODT K.;
HUM. REPROD. 8:635-641(1993).
-I- FUNCTION: MAY HAVE A ROLE IN NEUROENDOCRINE
-I- SUBUNIT: MONOMER.
                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 95010145.

JENSSN C.H., KROGH T.N., HOEJRUP P.,

LARSSON L.-I., ENGHILD J.J., TEISNER

EUR. J. BIOCHEM. 225:83-92(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-ADRENAL GLAND;
MEDLINE; 93179372.
LABORDA J., SAUSVILLE
                                                                                                                                                    ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-AMNIOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-AMNIOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 24-383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOCHIM. BIOPHYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
EUTHERIA; PRIMATES.
                                                                                                                                                                         ANTIGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEE Y.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95226449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-PLACENTA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
AND ADRENAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . BIOL. CHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLRNLCSSNYHGKRCNRYCIA-NAKL-HWECSTHGVRRCSAGWSGEDCSNP::| | | | | :| | : | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFRVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIP
                                                                                                                                                                    ; PS00010; ASX_HY
; PS00022; EGF_1;
; PS01186; EGF_2;
; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93273893
EC.
SPLICING.
1 23
24 383
24 303
34 303
327
3327
383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELMAN L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.7%;
larity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JSVILLE E.A., HOFFMAN 268:3817-3820(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLUID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLUID;
                                                                                                                                                                                           : ASX_HYDROXYL;
: EGF_1; 5.
: EGF_2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32, CAREATED)
33, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
N PRECURSOR (CONTAINS: FETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOFFMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFFMAN T., LABORDA J
1261:223-232(1995).
                                                                                                                                                                         EGF-LIKE DOMAIN; REPEAT; GLYCOPROTEIN; SIGNAL;
         DELTA-LIKE PROTEIN.
FETAL ANTIGEN 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOFFMAN T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
9; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116; DB 1;
No. 1.28e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLAUSEN P.P.,
B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTARIO V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTIGEN 1) (FA1) (DLK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .8.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKJODT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MADSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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-:- SIMILARITY: WITH OTHER BETA CHAINS FROM THE INTEGRIN FAMILY OF CELL-SURFACE RECEPTOR.

EMBL, M35198; G186507; ...

EMBL, A3669; E199078; ...

R EMBL, A37057; ...

R EMBL, A37057; ...

R EMBL, A37057; ...

R PIR; A37057; ...

R PROSITE; PS00243; INTEGRIN_BETA; 3.

R PROSITE; PS00243; INTEGRIN_BETA; 3.

R PROSITE; PS0186; EGF_1; UNKNOWN_2.

R PROSITE; PS0186; EGF_2; UNKNOWN_1.

R PROSITE; PS01186; EGF_2; UNKNOWN_1.

R PROSITE; PS01186; EGF_2; UNKNOWN_1.

R TYPERACELLULAR MATRIX; CYTOSKELETON; SIGNAL.

I SIGNAL
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-S28GC / AB972;

SUDINSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,

FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J.,

KUCABA T., HALLSWORTH K., HAWKINS J., HILLIER L., JIER M.,

JOHNSON D., JOHNSTON L., LANGSTON Y., LATREILLE P., LE T.,

MARDIS E., MENEZES S., MILLER N., NHAN M., PAULEY A., PELUSO D.,

RIFKEN L., RILES L., TAICH A., TREVASKIS E., VIGNATI D.,

WILCOX L., WOHLDMAN P., VAUDIN M., WILSON R., WATERSTON R.;

SUGMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                            INTEGRIN BETA-6.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL:
CYTOPLASMIC (POTENTIAL).
CYSTEINE-RICH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
G -> R (IN REF. 2).
81429BE0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101; DB 1; 1
Pred. No. 5.87e-03;
9; Mismatches 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                539 CDNFSCVRHKGLLCGGNGDC-DCGECVCRSGWTGEYCN 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CHITIN DEACETYLASE 2 PRECURSOR (EC 3.5.1.41).
CDA2 OR YLR307W OR L2142.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85975 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 5.8%;
Local Similarity 36.8%;
les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                           18
788
707
730
788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158
788 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
MEDLINE; 97279228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDA2_YEAST
Q06702;
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SHEPPARD D., ROZZO C., STARR L., QUARANTA V., ERLE D.J., PYTELA R.;
J. BIOL. CHEM. 265:11502-11507(1990).
[2]
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KRISSANSEN G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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-!- FUNCTION: INTEGRINS ARE A LARGE FAMILY OF CELL SURFACE
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MISSING (IN A SHORT FORM).
MISSING (IN CLONE HDLKAAG).
QP -> HV (IN REF. 1).
G -> D (IN REF. 3).
W; 9EEE3FIF CRC32;
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Pred. No. 8.66e-03;
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EGF-LIKE 4.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
BY SIMILARITH 
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Local Similarity 32.6%;
les 14; Conservative
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MEDLINE; 90307659.
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SPECHT C.A., ROBBINS P.W.;
YEAST 13:327-336(1997)
-!- FUNCTION: HYDROLYSES THE N-ACETAMIDO GR
-!- GLUCOSAMINE RESIDUES IN CHITIN +
-!- CATALYTIC ACTIVITY: CHITIN + H(2)0 - CH
-!- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIV
-!- SIMILARITY: TO OTHER POLYSACCHARIDE DEA
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J. BIOL. CHEM. 265:11502-11507(1990).

-i- FUNCTION: INTEGRINS ARE A LARGE FAMILY OF CELL SURFACE
GLYCOPROTEINS THAT MEDIATE CELL TO CELL TO MATRIX ADHESION.

-i- SUBCULT: DIMER OF AN ALPHA AND BETA SUBUNIT.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
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P18563;
01-NOV-1990
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EMBL; A26611; E199079; -.
PIR; B37057; B37057.
HSSP; P04355; 2MRT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (REL. 16,
01-NOV-1990 (REL. 16,
01-OCT-1996 (REL. 34,
                                                                                                                                                                                                                                                                      PROSITE;
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Similarity 25.0%;
13; Conservative
                                                                                                                                                                                                                                                 PS00243; INTEGRIN_BETA; 2.
PS00022; EGF_1; UNKNOWN_2.
PS01186; EGF_2; UNKNOWN_1.
; CELL ADHESION; TRANSMEMBRANE;
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LML2_CAEEL STANDARD; PRT; 3672 AA.

Q21313;

01-NOV-1997 (REL. 35, CREATED)

01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

LAMININ-LIKE PROTEIN K08C7.3 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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-!- SIMILARITY: CONTAINS 21.5 LAMININ EGF-LI
-!- SIMILARITY: CONTAINS ONE LAMININ DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BERKS M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAENORHABDITIS ELEGANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAZOA;
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1461
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EGF_2; 4.
  808
14605
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331
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39.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACOELOMATES; NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GENBANK/DDBJ DATA BANKS.

S ONE LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

S 21.5 LAMININ EGF-LIKE DOMAINS.

S ONE LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W.
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Pred. No.
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8; M
LAMININ EGF-LIR
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EGF-LIKE DOMAIN;
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                                                                                                                                                                                                                                            Y N-TERMINAL
Y EGF-LIKE 2.
Y EGF-LIKE 2.
N EGF-LIKE 3.
N EGF-LIKE 5.
N EGF-LIKE 5.
N EGF-LIKE 6.
N EGF-LIKE 6.
N EGF-LIKE 10.
N EGF-LIKE 11.
                                                                              | DOMAIN IV.
| EGF-LIKE 1
| EGF-LIKE 1
| EGF-LIKE 1
| EGF-LIKE 2
| EGF-LIKE 2
| EGF-LIKE 2
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                                                                                                                                                                                                                                                                                                                                                      (INCOMPLETE)
                                                                                                                                                                                                                                                   (N-TERMINAL).
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Matches 1
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P34418;
O1-FEB-1994 ()
O1-FEB-1994 ()
O1-JUN-1994 ()
HYPOTHETICAL
F42H10.5
                                                                                                                                                                      CARBOHYD
CARBOHYD
CONFLICT
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DISULFID
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DOMAIN
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ANTIGEN;
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DOMAIN
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DOMAIN
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18; Conse
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; PS00022; EGF_1;
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(REL.
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L 89.2
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llarity 30.5%;
Conservative
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             ELEGANS
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; EGF_1; 5.
; EGF_2; 6.
                          28,
29,
7D
                                                                                                                                                                ACCELOMATES;
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                         , CREATED)
, LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDAT
, PROTEIN F42H10.5 IN CH
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
                                                                                                            Score
Pred.
9; M
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EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 6.
BY SIMILARITY
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VLGTVAIVFLNKCETWVSNLRYNHTFRKKKNLLLQYNSGEE
LAVNIIFPEKIDMTTFNKEAGDEEI -> CWAPWPSSFSTS
AKPGCPTCATTTCFARRRISCCSITAARSWRSISSSPRRLT
                                                                                                                                     (IN REF. 2).
8630456D CRC32;
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DELTA-LIKE PROTEIN.
                                                          PRT;
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                                                                                                            re 95; DB 1; Le
1. No. 5.81e-02;
Mismatches 30
        NEMATODA;
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                          UPDATE)
IN CHROMOSOME
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        SECERNENTEA; RHABDITIDA.
                                                                                                             30;
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Best Local
DOMAIN
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CHAIN
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BONFIELD J., BURTON J., CONDELL M., COPSEY T., COOPER J., COULSON I
CRAXTON M., DEAR S., DU Z., DURBIN R., FRAVELLO A., FRASER A.,
FULTON L., GARNURER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.
PARSONS J., PERCY C., RIFKEN L., ROOPA A., SONNDARS C., SHOWNKEEN
SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
                                                                                                                                                                                                 PIR; A39490; A39490.
HSSP; Q99405; 1MPT.
MIM; 167405; -.
                                                                                                                                                                                                                                                                                                                                                                                                       DNA CELL BIOL. 10:757-769(1991)
-!- SUBCELLULAR LOCATION: SECRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 92075167.
KIEFER M.C., TUCKER J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAC4_HUMAN STANDARD; PRT; 969 AA P29122;
01-DEC-1992 (REL. 24, CREATED) 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDAT SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (E
                                                                                             SIGNAL
                                                                                                              ALTERNATIVE
                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                             +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMOH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NATURE 368:32-38(1994).
EMBL; L08403; G289681;
WORMPEP; F42H10.5; CE00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WATERSON R., WATSON A., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              676
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                                                                                                                                                                                                                                                  LYS-471.
- SIMILARITY: BELONGS TO SUBTILASE FAMILY. HICK M80482; G189532; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECIFICITY: WIDESPREAD, WITH COMPARATIVELY HIGHER
IN THE LIVER. PACE4.1 WAS ONLY FOUND IN THE LIVER.
ALTERNATIVE PRODUCTS: TWO VARIANTS SEEM TO BE PRODUCED BY
ALTERNATIVE SPLICING OF A SINGLE GENE. THEY DIFFER AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SY-W 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCETALAIYGDLFQSITGNSSESK-ENIVNQYFDEISSTTSVESMFMLRTFGNPMQAPL
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5
                                                                                                                                               PS00137;
PS00138;
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Similarity 23.4%;
                                                                                                                                                                                   PS00136;
                                                                                                                            S00136; SUBTILASE_ASP;
S00137; SUBTILASE_HIS;
S00138; SUBTILASE_SER;
SERINE PROTEASE; GLYCO
 SPLICING; R
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149
150 969
150 969
695 969
205 205
246 246
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E.,
                                                                                                              REPEAT
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                                                                                                                                                                                                                                                                          PEPTIDASE FAMILY S8; F
SIMILARITY WITH OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 94;
Pred. No. 8
16; Mismat
POTENTIAL.

POTENTIAL.

POTENTIAL.

SUBTILISIN-LIKE PROTE

CYS-RICH REGION.

CHARGE RELAY SYSTEM (

CHARGE RELAY SYSTEM (
                                                                                                                              GLYCOPROTEIN; ZYMOGEN; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽.,
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SEEM TO BE PRODUCED BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           X.E.,
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                                                         PROTEASE
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R FURIN-LIKE EN
 (BY SIMILARITY). (BY SIMILARITY).
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P SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-S288C / AB972;

STRAIN-S288C / AB972;

A DIETRICH F.S., MULLICAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R., AULLES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M., AULLES E., DUNCAN M., GURANN E., LASHEARI D., LEW H., LIN D., HYMAN R., KAYSER A., KOMP C., LASHEARI D., LEW H., LIN D., MOSEDALE D., NAKAHARA K., NAMATH A., NORGREN R., OEFNER P., OH C., A PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN T., SMITH V., A TAYLOR P., WEI Y., YELYON M., BOTSTEIN D., DAVIS R.W.; SUBMITTED (DEC-1994) TO EMBLYGENBANK/ODBJ DATA BANKS.

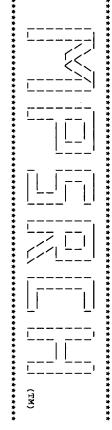
C -!- FUNCTION: HIGH-AFFINITY PERMEASE FOR ARGININE.

C -!- SUBCLIULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

C -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID
                                                                                                                                                                                                    ,;
                                                                                                                                                                                                     Gaps
CHARGE RELAY SYSTEM (BY SIMILARITY).
CELL ATTACHMENT SITE (POTENTIAL).
5 X TANDEM REPEATS, CYS-RICH.
                                                                                                                               K -> KGAAVAFWWTIGWPWNV (IN PACE4.1).
MISSING (IN PACE4.1).
; 1FE74A29 CRC32;
                                                                                                                                                                                                     ;
                                                                                                                                                                             Score 94; DB 1; Length 969;
Pred. No. 8.43e-02;
6; Mismatches 19; Indels
                                                                                                                                                                           Length 969
                                                                                                                                                                                                                          733 CPLGYFGDTAARRCR-RCHK-GCETCSSRAATQCLSCRRGFYHH 774
                                                                                                                                                                                                                                       184 CDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCH 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                    13-AUG-1987 (REL. 05, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                590 AA
                                                                                             POTENTIAL. POTENTIAL.
                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOFFMAN W.;
J. BIOL. CHEM. 260:11831-11837(1985)
                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                       106419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE, 88165106.
AHMAD M., BUSSEY H.;
CURR. GENET. 10:587-592(1986).
                                                                                                                                                                             Query Match 5.4%;
Best Local Similarity 38.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                     969 AA;
                                                                                                                                                                                                                                                                                                                                                        ARGININE PERMEASE.
CAN1 OR YELO63C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 86008235.
                                                                                                                                                                                                                                                                                    LT 15
CAN1_YEAST
P04817;
                                                                      REPEAT
REPEAT
CARBOHYD
CARBOHYD
                                                                                                                               VARSPLIC
VARSPLIC
SEQUENCE
  ACT_SITE
                                                                                                                      CARBOHYD
                          DOMAIN
                                               REPEAT
REPEAT
                                       REPEAT
   21111111111118
                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                 δλ
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FT TRANSMEM 494 518 POTENTIAL.
FT TRANSMEM 525 548 POTENTIAL.
FT DOMAIN 549 590 HYDROPHILIC.
FT CONFLICT 534 534 I -> V (IN REF. 1).
SQ SEQUENCE 590 AA; 65785 MW; 74DCD8FC CRC32;
Query Match 5.3%; Score 92; DB 1; Length 590;
Best Local Similarity 37.0%; Pred. No. 1.76e-01;
Matches 10; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Db 157 SQRFLSPAFGAANGYMYWFSWAITFAL 183
:|||::||::||:||:||:||
```

Search completed: Fri Jun 12 12:05:13 1998 Job time : 20 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 12 12:05:30 1998; MasPar time 12.66 Seconds 764.729 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-083-590A-2 (1-230) from US08083590A.pep (2 of 2) 1734

Sequence: 1 MHWIKCLLTAFICFTVIVQV......ETGEIICLTGWQGDYCHIPK 230

Scoring table: PAM 150 Gap 11

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 42.709; Variance 68.565; scale 0.623

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 20 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | ω | N | 1 | ::::: | Result |
|----------------------|------------------------|------------------------|------------------------|------------------------|---------------------|------------------------|------------------------|------------------------|-----------|------------------------|-----------------------|-----------------------|-----------------|------------|-----------|------------------------|-----------------------|------------------------|-------------|--------------------------|
| 1127 | 130 | 137 | 212 | 249 | 485 | 516 | 553 | 573 | 587 | 589 | 589 | 590 | 593 | 734 | 751 | 769 | 775 | 1734 | | Score |
| 6.5 | 7.5 | 7.9 | 12.2 | 14.4 | 28.0 | 29.8 | 31.9 | 33.0 | 33.9 | 34.0 | 34.0 | 34.0 | 34.2 | 42.3 | 43.3 | 44.3 | 44.7 | 100.0 | 1 1 1 1 1 1 | Query |
| 544 3 | 379 | 403 | 139 | 585 | | | 1212 | 1193 | 1218 | 1227 | 1218 | 1218 | | 721 | 723 | 717 | 728 | 832 | | Query Match Length DB |
| ww | w | ω | 10 | 10 | 10 | 12 | 12 | 12 | N | 2 | N | N | 10 | 12 | N | 12 | 12 | ω | ! | B |
| Q17377 Q19480 | Q19922 | 018375 | P97606 | 035675 | P97607 | P79941 | 042347 | Q90819 | 015122 | P78504 | 014902 | Q15816 | Q63722 | Q91902 | 000548 | P87357 | Q90656 | 099108 | | I |
| ARG-1. F15B9.3. | STRONG SIMILARITY TO C | C901 PROTEIN (FRAGMENT | JAGGED2 PRECURSOR (FRA | M-DELTA-LIKE 3 GENE PR | JAGGED2 (FRAGMENT). | NOTCH LIGAND X-DELTA-2 | C-SERRATE-2 (FRAGMENT) | C-SERATE-1 PROTEIN (FR | JAGGED1. | JAGGED 1 (TRANSMEMBRAN | TRANSMEMBRANE PROTEIN | TRANSMEMBRANE PROTEIN | JAGGED PROTEIN. | X-DELTA-1. | DELTA. | DELTAD TRANSMEMBRANE P | TRANSMEMBRANE PROTEIN | NEUROGENIC LOCUS DELTA | | Description |
| 3.28e-07 1.60e-04 | 9.11e-08 | 4.36e-09 | 1.40e-24 | 8.14e-33 | 2.76e-89 | 5.51e-97 | 3.16e-106 | 3.04e-111 | 9.19e-115 | 2.88e-115 | 2.88e-115 | 1.62e-115 | 2.84e-116 | 4.73e-152 | 2.14e-156 | 5.29e-161 | 1.54e-162 | 0.00e+00 | | Pred. No. |

| 444 | 40 | 3 3 9 8 | 37 | ω | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 |
|------------------|---|--|--|---|--|---|--|--|---|--|--|---|--|--|---|--|--|---|
| 91 | 90 91 | 93 94 | 93 | 94 | 96 | 95 | 96 | 96 | 96 | 95 | 95 | 97 | 97 | 103 | 102 | 105 | 105 | 108 |
| л N N I | л (л () () | 5.4 4.4 | 5.4 | 1 51 | | | | | | | | | | | | | | 6.2 |
| 9885 | 148 296 | 4006 4135 | 2531 | | 4289 | 2531 | 2447 | 781 | 750 | 385 | 141 | 3704 | 220 | 788 | 263 | 1476 | 387 | 144 |
| 10 | 10 9 | 10 4 | ωE | 50 | ν | ω | 12 | 12 | N | 10 | 9 | ω | 10 | 12 | N | 12 | w | 12 |
| Q54468 Q52030 | Q45805 | 035452 018977 | Q21980 | 800900 | P78530 | 016004 | 013149 | Q92071 | Q08424 | 062208 | 006303 | P91904 | Q63404 | Q07012 | Q99734 | Q90285 | Q20681 | 012973 |
| ÓН | 14 | TENASCIN-X. | SIMILAR TO TENASCIN. | NOTCH PROTEIN HOMOLOG | TENASCIN X. | Ю | NOTCH 2 (FRAGMENT). | INTEGRIN BETA3. | TENASCIN-X PRECURSOR (| DERIVED | 14.4 KD | • | (CLONE REM4) ORF (FRAG | PLATELET MEMBRANE GLYC | NOTCH2 TRANSMEMBRANE P | PUTATIVE EXTRACELLULAR | F52H3.3. | SERRATE-2 (FRAGMENT). |
| 4.30e-01 | 6.09e-01 | 2.12e-01 1.49e-01 | 2.12e-01 | 1.49e-01 | 7.22e-02 | 1.04e-0 | 7.22e-0 | 7.22e-02 | 7.22e-02 | 1.04e-0 | 1.04e-0 | 5.02e-0 | 5.02e-02 | 5.34e-Q | 7.81e-03 | 2.49e-03 | 2.49e-03 | 7.76e-04 |
| | 91 5.2 885 9 Q54468 N-ACETYL-BETA-D-GLUCOS 01 5.2 833 10 Q52030 BDDBBCTEIN CONVERTAGE | 90 5.2 148 9 Q45805 PUTATIVE REGULATORY PR 6 91 5.2 296 10 035171 PACE4 (FRAGMENT). 4 91 5.2 896 10 054468 N-ACETYL-BETA-D-GLUCOS 4 91 5.2 832 10 062030 DECEMBER 1 CONVERTAGE 4 | 93 5.4 4006 10 035452 TENASCIN X. 94 5.4 4135- 4 018977 TENASCIN X. 90 5.2 148 9 045805 PUTATIVE REGULATORY PR 6 90 5.2 296 10 035171 PACE4 (FRAGMENT). 91 5.2 296 10 035171 PACE4 (FRAGMENT). 91 5.2 885 9 054468 N-ACETYL-BETA-D-GLUCOS 4 01 5.2 032 10 062030 PRODECTEIN CONVENTAGE | 93 5.4 24/0 10 03516 CELL SURFACE PROTEIN. 1 93 5.4 2531 3 021980 SIMILAR TO TENASCIN. 2 93 5.4 4006 10 035452 TENASCIN X. 2 94 5.4 4135- 4 018977 TENASCIN-X. 2 95 5.2 148 9 045805 PUTATIVE REGULATORY PR 6 97 5.2 296 10 035171 PACE4 (FRAGMENT). 4 98 5.2 885 9 054468 N-ACETYL-BETA-D-GLUCOS 4 98 5.2 885 9 054468 N-ACETYL-BETA-D-GLUCOS 4 99 5.2 885 9 054468 N-ACETYL-BETA-D-GLUCOS 4 | 94 5.4 1203 10 006008 NOTCH PROTEIN HOWOLOG 1 94 5.4 2470 10 035515 CELL SURFACE PROTEIN. 1 93 5.4 2531 3 021980 SIMILAR TO TENASCIN. 2 93 5.4 4006 10 035452 TENASCIN X. 2 94 5.4 4135- 4 018977 TENASCIN-X. 1 94 5.2 148 9 045805 PUTATIVE REGULATORY PR 6 95 5.2 148 9 045805 PACE4 (FRAGMENT). 4 91 5.2 296 10 035171 PACE4 (FRAGMENT). 4 91 5.2 885 9 054468 N-ACETYL-BETA-D-GLUCOS 4 91 5.2 885 9 054468 N-ACETYL-BETA-D-GLUCOS 4 91 5.2 885 9 054468 N-ACETYL-BETA-D-GLUCOS 4 | 96 5.5 4289 2 P78530 TENASCIN X. 94 5.4 1203 10 Q05008 NOTCH PROTEIN HOMOLOG 1 94 5.4 2470 10 Q35516 CELL SURFACE PROTEIN. 1 93 5.4 2531 3 Q21980 SIMILAR TO TENASCIN. 2 93 5.4 4006 10 Q35452 TENASCIN X. 94 5.4 4135- 4 Q18977 TENASCIN X. 94 5.2 148 9 Q45805 PUTATIVE REGULATORY PR 6 91 5.2 296 10 Q35171 PACE4 (FRAGMENT). 4 91 5.2 885 9 Q54468 N-ACETYL-BETA-D-GLUCOS A 91 5.2 885 9 Q54468 N-ACETYL-BETA-D-GLUCOS A 91 5.2 885 9 Q54468 N-ACETYL-BETA-D-GLUCOS A 91 5.2 885 9 Q54468 N-ACETYL-BETA-D-GLUCOS A | 95 5.5 2531 3 016004 NOTCH HOMOLOG. 1 96 5.4 4209 2 P78530 TENASCIN X. 7 94 5.4 1203 10 Q06008 NOTCH PROTEIN HOMOLOG 1 94 5.4 2470 10 035516 CELL SURFACE PROTEIN. 1 94 5.4 2531 3 Q21980 SIMILAR TO TENASCIN. 2 93 5.4 4006 10 035452 TENASCIN X. 7 94 5.4 4006 10 035452 TENASCIN X. 9 95 5.4 4006 10 035477 TENASCIN X. 1 96 5.2 148 9 Q45805 PUTATIVE REGULATORY PR 6 97 5.2 885 9 Q45468 N-ACETYL-BETA-D-GLUCOS 4 98 5.2 885 9 Q54468 N-ACETYL-BETA-D-GLUCOS 4 99 5.2 885 9 Q54468 N-ACETYL-BETA-D-GLUCOS 4 91 5.2 885 9 Q54468 NOTEL NO | 96 5.5 2447 12 013149 NOTCH 2 (FRAGMENT). 7 95 5.5 2231 3 016004 NOTCH HOMOLOG. 7 96 5.5 4289 2 P78530 TENASCIN X. 7 96 5.4 1203 10 006008 NOTCH PROTEIN HOMOLOG 1 94 5.4 2470 10 035516 CELL SURFACE PROTEIN. 2 93 5.4 2470 10 035516 SIMILAR TO TENASCIN X. 2 93 5.4 4006 10 035452 TENASCIN X. 2 94 5.4 4135- 4 018977 TENASCIN X. 2 95 5.2 148 9 045805 PUTATIVE REGULATORY PR 6 96 5.2 148 9 045805 PUTATIVE REGULATORY PR 6 97 5.2 296 10 035171 PACE4 (FRAGMENT). 4 98 5.2 296 10 035171 PACE4 (FRAGMENT). 4 99 5.2 885 9 054468 N-ACETYL-BETA-D-GLUCOS A 91 5.2 885 9 054468 N-ACETYL-BETA-D-GLUCOS A 91 5.2 885 9 054468 N-ACETYL-BETA-D-GLUCOS A | 96 5.5 781 12 Q92071 INTEGRIN BETA3. 7 96 5.5 2447 12 Q13149 NOTCH 2 (FRAGMENT). 7 95 5.5 2531 3 Q16004 NOTCH HOMOLOG. 1 96 5.5 4289 2 P78530 TENASCIN X. 7 94 5.4 1203 10 Q06008 NOTCH PROTEIN HOMOLOG 1 94 5.4 2470 10 Q35516 CELL SURFACE PROTEIN. 1 94 5.4 2470 10 Q35516 CELL SURFACE PROTEIN. 2 93 5.4 4270 10 Q35452 TENASCIN X. 7 93 5.4 4006 10 Q35452 TENASCIN X. 7 94 5.4 4135- 4 Q1980 TENASCIN X. 7 95 5.2 44135- 4 Q45805 PUTATIVE REGULATORY PR 6 96 5.2 188 9 Q45805 PUTATIVE REGULATORY PR 6 97 5.2 885 9 Q54468 N-ACETYL-BETA-D-GLUCOS A 98 5 Q Q5200 PRODEOTEIN CONVENTAGE A 99 5 Q Q5200 PRODEOTEIN CONVENTAGE A 91 5 Q Q32 10 Q52030 PRODEOTEIN CONVENTAGE A | 96 5.5 750 2 008424 TENASCIN-X PRECURSOR (796 5.5 750 2 008424) 96 5.5 751 2 092071 INTEGRIN BETA3. 96 5.5 2447 12 013149 NOTCH 2 (FRAGMENT). 795 5.5 2531 3 016004 NOTCH HOMOLOG. 796 5.5 4289 2 P78530 NOTCH PROTEIN HOMOLOG 1796 5.4 1203 10 006008 NOTCH PROTEIN HOMOLOG 1796 5.4 2470 10 035516 CELL SURFACE PROTEIN. 193 5.4 2531 3 021980 SIMILAR TO TENASCIN. 293 5.4 4006 10 035452 TENASCIN X. 94 5.4 4135-4 018977 TENASCIN X. 95 5.2 148 9 045805 PUTATIVE REGULATORY PR 691 5.2 296 10 035171 PACE4 (FRAGMENT). 40 0520468 N-ACETYL-BETA-D-GLUCOS A 0520468 N-AC | 95 5.5 385 10 062208 STROMAL CELL DERIYED P 96 5.5 781 12 092071 INTEGRIN BEPRAS 96 5.5 781 12 092071 INTEGRIN BEPRAS 96 5.5 2447 12 013149 NOTCH 2 (FRAGMENT). 95 5.5 2531 3 016004 NOTCH HOMOLOG. 96 5.5 4289 2 P78530 TENASCIN X. 96 5.4 1203 10 006008 NOTCH PROTEIN HOMOLOG 97 5.4 2470 10 035516 CELL SURFACE PROTEIN. 98 5.4 2470 10 035516 SIMILAR TO TENASCIN X. 98 5.4 2470 10 035452 TENASCIN X. 99 5.4 4135- 4 018977 TENASCIN X. 90 5.2 148 9 045805 PUTATIVE REGULATORY PR 90 5.2 148 9 045805 PUTATIVE REGULATORY PR 91 5.2 296 10 035171 PACE4 (FRAGMENT). 91 5.2 085 9 054468 N-ACETYL-BETA-D-GLUCOS 91 5.2 085 9 054468 N-ACETYL-BETA-D-GLUCOS | 95 5.5 141 9 006303 HYPOTHETICAL 14.4 KD P 1 95 5.5 345 10 062208 STROMAL CELL DERIVED P 1 96 5.5 750 2 008424 TENASCIN-X PRECURSOR (7 96 5.5 781 12 092071 INTEGRIN BETA3. 7 96 5.5 2447 12 013149 NOTCH 2 (FRAGMENT). 7 95 5.5 2531 3 016004 NOTCH HOMOLOG. 7 96 5.5 4289 2 P78530 TENASCIN X. 7 94 5.4 1203 10 006008 NOTCH HOMOLOG 1 94 5.4 2470 10 035516 CELL SURFACE PROTEIN. 93 5.4 2470 10 035516 CELL SURFACE PROTEIN. 93 5.4 2470 10 035452 TENASCIN X. 93 5.4 4006 10 035452 TENASCIN X. 94 4135- 4 018977 TENASCIN X. 90 5.2 148 9 045805 PUTATIVE REGULATORY PR 6 15 2 296 10 035171 PACE4 (FRAGMENT). 4 15 | 97 5.6 3704 3 P91904 HAMININ ALPHA. 95 5.5 141 9 006303 HYPOTHETICAL 14.4 KD P 95 5.5 385 10 Q62208 STROWAL CELL DERLYED P 96 5.5 750 2 Q08424 TENASCIN-X PRECURSOR (7 96 5.5 781 12 Q92071 INTEGRIN BETA3. 96 5.5 2447 12 013149 NOTCH 2 (FRAGMENT). 7 95 5.5 2531 3 016004 NOTCH HOMOLOG. 7 96 5.5 4289 2 P78530 TENASCIN X. 96 5.5 4289 2 P78530 NOTCH HOMOLOG. 7 97 5.4 2470 10 035515 CELL SURFACE PROTEIN. 1 98 5.4 2470 10 035515 CELL SURFACE PROTEIN. 2 99 5.4 2470 10 035452 TENASCIN X. 99 5.4 4135- 4 008977 TENASCIN X. 90 5.2 148 9 Q45805 PUTATIVE REGULATORY PR 90 5.2 148 9 Q45805 PUTATIVE REGULATORY PR 91 5.2 296 10 035171 PACE4 (FRAGMENT). 4 91 5.2 296 10 035171 PACE4 (FRAGMENT). 4 91 5.2 032 10 062030 PRODECTEIN CONVERTAGE | 97 5.6 220 10 063404 (CLONE REMA) ORF (FRAG 5 97 5.6 3704 3 P91904 LAMININ ALPHA. P1 95 5.5 141 9 006303 HYPOTHETICAL 14.4 KD P 1 95 5.5 385 10 062208 STROMAL CELL DERIVED P 1 96 5.5 750 2 008424 TENASCIN-X PRECURSOR (7 781 12 092071 INTEGRIN BETA 3. 96 5.5 2447 12 013149 NOTCH 2 (FRAGMENT). 7 95 5.5 2531 3 016004 NOTCH HOMOLOG. 7 96 5.5 4289 2 P78530 TENASCIN X. 94 5.4 1203 10 006008 NOTCH PROTEIN HOMOLOG 94 5.4 2470 10 035516 CELL SURFACE PROTEIN. 93 5.4 2470 10 035516 CELL SURFACE PROTEIN. 93 5.4 4006 10 035452 TENASCIN X. 99 5.2 148 9 045805 FUNDAMENTORY PR 6 15 2 296 10 035171 PACE4 (FRAGMENT). 4 10 035458 POCEAUCAS PROTEIN OF CONVENTANCE A 1 10 006008 PACE4 (FRAGMENT). 4 10 006008 | 103 5.9 788 12 Q07012 PLATELET MEMBRANE GLYC 5 97 5.6 3704 3 P91904 LAMININ ALPHA. 5 97 5.6 3704 3 P91904 LAMININ ALPHA. 5 97 5.6 3704 3 P91904 LAMININ ALPHA. 5 98 5.5 141 9 Q06303 STROMAL CELL DERIVED P 98 5.5 385 10 Q62208 STROMAL CELL DERIVED P 98 5.5 750 2 Q08424 TENASCIN-X PRECURSOR (98 5.5 781 12 Q92071 INTEGRIN BETA3. 7 98 5.5 2447 12 Q13149 NOTCH PCRAGMENT). 7 99 5.5 2531 3 Q16004 NOTCH HOMOLOG. 7 99 5.5 4289 2 P78530 TENASCIN X. 7 90 5.4 1203 10 Q06008 NOTCH PROTEIN HOMOLOG 1 94 5.4 1203 10 Q05016 CELL SURFACE PROTEIN. 2 93 5.4 2431 3 Q21980 SIMILAR TO TENASCIN X. 9 90 5.2 148 9 Q45805 PUTATIVE REGULATORY PR 6 91 5.2 296 10 Q35171 PACE4 (FRAGMENT). 4 91 5.2 296 10 Q35171 PACE4 (FRAGMENT). 4 91 5.2 296 10 Q5916 PROTEIN OUNDERSER A. 4 91 5.2 296 10 Q5916 PROTEIN OUNDERSER A. 4 91 5.2 296 10 Q5917 PACE4 (FRAGMENT). 4 91 5.2 296 10 Q5916 PROTEIN OUNDERSER A. 4 91 5.2 296 10 Q5916 PROTEIN OUNDERSER A. 4 91 5.2 296 10 Q5917 PACE4 (FRAGMENT). 4 | 102 5.9 263 2 099734 NOTCH TRANSMEMBRANE P 7 7 103 5.9 263 2 099734 CLONE REM4) OFF (FRAG 5 97 5.6 220 10 063404 (CLONE REM4) OFF (FRAG 5 97 5.6 3704 3 P91904 LAMININ ALPHA. 97 5.6 3704 3 P91904 LAMININ ALPHA. 97 5.5 345 10 065208 STROMAL CELL DERIVED P 195 5.5 345 10 065208 STROMAL CELL DERIVED P 196 5.5 750 2 008424 TENASCIN X PRECURSOR (7 7 7 112 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 105 6.1 1476 12 090285 PUTATIVE EXTRACELLULAR 2 2 099734 NOTCH2 TRANSMEMBRANE P 103 5.9 788 12 007012 PLATELET MEMBRANE P 2 099734 NOTCH2 TRANSMEMBRANE P 2 099734 NOTCH2 TRANSMEMBRANE P 2 0907012 PLATELET MEMBRANE ELYC 5 220 10 0630404 CCLONE REM4) ORF (FRAG 5 141 9 006303 HYPOTHETICAL 14.4 KD P 1 06303 HYPOTHETICAL 14.4 KD P 1 06304 HYPOT | 6.1 387 3 020681 F52H3.3. 6.1 1476 12 090285 PUTATIVE EXTRACELLULAR 2 9263 2 099734 NOTCH2 TRANSMEMBRANE P 7 5.9 788 12 007012 PLATELET MEMBRANE GLYC 5.6 3704 3 P91904 LAMININ RAPPIA. 5.5 141 9 006303 HYPOTHETICAL 14.4 KD P 1 5.5 750 2 008424 TENASCIN YERCURSOR (7 5.5 781 12 092071 INTEGRIN BETA3. 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 |

ALIGNMENTS

| 30000 K K K K K K K K K K K K K K K K K | 3888 8888 | 48888 | R R R R | P R R R R | 2 F R R R R R R R | 888 | DI DI | RESULT ID Q |
|--|---|---|---|-----------|---|--|--|---|
| -!- SIMILARITY: THE PROTEIN INCLUDES 9 EGF-LIKE REPEATS!- SIMILARITY: TO DROSOPHILA SERRATE PROTEIN (AC P18168), AND VERTEBRATE BLOOD COAGULATION FACTOR IX. EMBL; Y00222; G577774; ELYBASE; EBSO0000463; D1. DIFFERENTIATION; NEUROGENESIS; REPEAT; TRANSMEMBRANE; EGF-LIKE DOMAIN; GLYCOPROTEIN; SIGNAL. | OF EMBRYO IS ONE OF THE FIRST STEPS OF CNS DEVELOPMENT IN I THIS PROCESS IS UNDER CONTROL OF THE NEUROGENIC GENES. NOTCH AND SERRATE MAY INTERACT AT THE PROTEIN LEVEL, IT IS CONCEIVABLE THAT THE SERRATE DELTA PROTEINS MAY COMPETE CONCEIVABLE THAT THE NOTCH EDUCATION | DEVELOPMENT 110:905-914(1990). -i- FUNCTION: ESSENTIAL FOR PROPER DIFFERENTIATION OF ECTODERM. DL IS REQUIRED FOR THE CORRECT SEPARATION OF NEURAL AND EPIDERMAL CELL LINEAGES. -i- SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO THE INNER PART | HAENLIN M., KRAMATSCHEK B., CAMPOS-ORTEGA J.A.; | | SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-OREGON-R; TISSUE-EMBRYO; MEDLINE; 89196890. KOPCZYNSKI C.C., ALTON A.K., FECHTEL K., KOOH P.J., MUSKAVITCH M.A.T.; GENES DEV. 2:1723-1735(1988). | SOPHILA MELANOGASTER ARYOTA; METAZOA; ARI | 01-NOV-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-FEB-1997 (TREMBLREL. 02, LAST SANOTATION UPDATE) NEUROGENIC LOCUS DELTA PROTEIN PRECURSOR (VERSION 2). | LT 1 099108. PRELIMINARY; PRT; 832 AA. |

78 79

DOMAIN

REPEAT

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                                                                                                                                                                                                             61 ICLKHYQANVSPDPPCTYGGAVTPVLGSNSFQVPES -- FPDSSFTNPIPFAFGFTWPGTF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 SLIIEALHTDSTDDLSTENPDRLISRMTTQRHLTVGEEWSQDLQVGGRTELKYSYRFVCD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQCDCKTFFRVCLKHYQASVSP
                     19 QVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGRCLGSCKTRFRVCLKHYQATIDT
                                                                                         80 EPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPGTFSLIIEALHTDSP
                                                                                                                                                                                     DDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSYRFVCDEHYYGEGCSVFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRACHYDANIO RERIO (2EBRAFISH) (ZEBRA DANIO).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 19 POTENTIAL.
20 117 DELTAD TRANSMEMBRANE PROTEIN.
717 AA: 79061 MW; 5CC32ECA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 EHYYGEGCSVFCRPRDDTFGHFTCGERGEIICNSGWKGQYCTEP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-AAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DELTAD TRANSMEMBRANE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 44.3%; Score 769; DB 12; L
Best Local Similarity 46.0%; Pred. No. 5.29e-161;
Matches 103; Conservative 40; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MANN R.S., GRAY G.E., HENRIQUE D., ISH-HOROWICZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                        717 AA
                                                                                                                                                                                                                                                                              200 RPRDDRFGHFTCGERGEKVCNPGWKGQYCTEP 231
                                                                                                                                                                                                                                                                                                       198 RPRDDSFGHSTCSETGEIICLTGWQGDYCHIP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     723
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01-JUL-1997 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
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P87357
P87357;
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000548;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-SPINAL CORD;
MEDLINE: 9319507.
HENRIOUE D., ADAM J., MYAT A., CHITNIS A., LEWIS J., ISH-HOROWICZ D.;
NATURE 375:787-790(1995).
EMBL: U56590; G882412; -.
PROSITE: PS01187; EGF_CA; 2.
GLYCOPROTEIN; EGF_LIKE DOMAIN.
SEQUENCE 728 AA; 79861 MW; 7439F575 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CKTRFRVCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CKTRFRVCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSF 120
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Pred. No. 1.54e-162;
33; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1734; DB 3; Length 832; Pred. No. 0.00e+00;
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                                                                                    INTRACELLULAR (POTENTIAL).
9 EGF-TYPE REPEATS.
                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
GK -> ET (IN REF. 2).
A -> S (IN REF. 2).
G -> A (IN REF. 2).
T -> A (IN REF. 2).
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TRANSMEMBRANE PROTEIN C-DELTA-1.
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                        DELTA PROTEIN.
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POTENTIAL.
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Local Similarity 100.0%;
nes 230; Conservative
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Best Local Similarity 49.1%;
Matches 104; Conservative
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832 AA;
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Matches 10
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Best Loc
Matches
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EMBL; L42229; G807696; ---
PROSITE; PSO1187; EGF_CA; 2.
GLYCOPROTEIN; EGF-LIKE DOMAIN.
SEQUENCE 721 AA; 79922 MW; 0
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01-JAN-1996
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Q91902
Q91902;
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EMBL; AF003522; G2197069; -.
PROSITE; PS01187; EGF_CA; 1.
GLYCOPROTEIN; EGF-LIKE DOMAIN.
SEQUENCE 723 AA; 77956 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 95319503.
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HENRIQUE D., ADAM J., MYAT
NATURE 375:787-790(1995).
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    186
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    LNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIP
                                                                              SLIIEAIHADSADDLNTENPERLISRLATQRHLTVGEQWSQDLHSSDRTELKYSYRFVCD
                                                                                                                                                                                                                                                                     MLTLLVLSAVLCQISCSGLFELRLQEFVNKKGLLGNMNCCRPGSLASLQRC--ECKTFFR
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                                                                                                                                                                   CDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIP
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                                          EYYYGEGCSDYCRPRDDAFGHFSCGEKGEKLCNPGWKGLYCTEP
                                                                                                                                                                                                         ICLKHYQSNVSPEPPCTYGGAVTPVLGTNSFVVPESSN-ADPTFSNPIRFPFGFTWPGTF
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larity 46.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                   42.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05, C1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEWIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UI
LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                Score 734; DB 12;
Pred. No. 4.73e-152;
40; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 751; DB 2; I
Pred. No. 2.14e-156;
39; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROG).
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                                                                                                                                                                                                                                                                                                                                                                                                                   028040EF CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISH-HOROWICZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEWIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UPDATE)
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                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISH-HOROWICZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINTNER
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RESULTION OF THE PROPERTY OF T
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Query Match
Best Local S
Matches 8
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Best Local
                                                                                                                SEQUENCE FROM N.A.

GRAY G.E., MANN R.S., MITSIADIS E., HENRIQUE D.,
GRAY G.E., MANN R.S., MITSIADIS E., HENRIQUE D.,
ISH-HOROWICZ D., ARTAVANIS-TSAKONAS S.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA B#
EMBL; U61276; G1438937; -.
PROSITE; PS01187; EGF_CA; 8.
TRANSMEMBRANE; GLYCOPROTEIN; EGF-LIKE DOMAIN.
TRANSMEMBRANE; GLYCOPROTEIN; EBD64FED CRC32;
SEQUENCE 1218 AA; 133739 MW; E8D64FED CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          063722; P706:
063722; P706:
01-NOV-1996
01-FEB-1997
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q15816;
Q15816;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 95211842.
LINDSELL C.E., SHAWBER C.J.,
CELL 80:909-917(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01. NOV-1996 (TREMBLREL. 01, CREATED)
01.NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01.JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDAT
TRANSMEMBRANE PROTEIN JAGGED 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L38483; G1492111; -.

PROSITE; PSO1187; ESF CA: 8.

GLYCOPROTEIN; ESF-LIKE DOMAIN

SEQUENCE 1219 AA; 134325 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JAGGED PROTEIN.
RATTUS NORVEGICUS (RAT)
EUKARYOTA; METAZOA; CHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 95211842.
LINDSELL C.E., SHAWBER
CELL 80:909-917(1995).
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h 34.0%;
Similarity 39.0%;
87; Conservative
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(TREMBLREL.)
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larity 38.6%;
Conservative
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Score
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50; N
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53; M
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LAST ANNOTATION
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re 590; DB 2; Le
d. No. 1.62e-115;
Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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No. 2.84e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1218
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                                                                    1218;
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SEQUENCE
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                                                                                                                                                                           FKVCLKEYQSRVTAGGPCSFGSGSTPVIGGNTFNLKAS-RGNDR---NRIVLPFSFAWPR 130
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FRVCLKHYQATIDITSQCTYGDVITPILGENSVNLTDAQRFQNRGFTNPIQFPFSFSWPG 124
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                                                                                                        FRVCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWPG 124
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINDSELL C.E., SHAWBER C.J., BOULTER J., WEINMASTER G.;
CELL 80:909-917(1995).
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SEQUENCE FROM N.A.,
BASH J., ZONG W.-X., GELINAS C.;
BASH J., ZONG W.-X., GELINAS C.;
SUBHITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF028593; G2599082; ...
PROSITE; PS01187; EGF CA; 8.
TRANSMEMBRANE; GLYCOPROTEIN; EGF-LIKE DOMAIN.
FROIENCE 1218 AA; 133798 MW; 07B97EE3 CRC32;
                                                                                                                                                                                                                                        DDYYYGFGCNKFCRPRDDFFGHYACDQNGNKTCMEGWMGPECN 230
                                                                                                                                                                                                                                                            DINYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCH 227
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TRANSMEMBRANE PROTEIN JAGGED 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
JAGGED 1 (TRANSMEMBRANE PROTEIN JAGGED).
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                                                                                                                                                                                                                                                                                                                                                                     PRT; 1218
                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 95211842.
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014902
014902;
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P78504;
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1227 AA; 134770 MW; 5D300881 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKVCLKEYQSRVTAGGPCSFGSGSTPVIGGNTFNLKAS-RGNDR---NRIVLPFSFAWPR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 TFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTC 184
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1227;
                                                                                                                                                                                                                   NGUYEN F., MONTESANO
                                        .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
ODA T., ELKAHLOUN A.G., PIKE B.L., OKAJIMA K., KRANTZ
PICCOLI D.A., MELTZER P.S., SPINNER N.B., COLLINS F.S.
CHANDRASEKHRARAPA S.G.,
NAT. GENET. 0:0-0(1997).
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
LI L., DENG Y., BANTA A.B., HOOD L.;
SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 DDYYYGFGCNKFCRPRDDFFGHYACDQNGNKTCMEGWMGPECN 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 589; DB 2; Lei
Pred. No. 2.88e-115;
52; Mismatches 75;
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                                                                                                                                                                         SEQUENCE OF 14-1227 FROM N.A.
MEDLINE; 97115768.
ZIMRIN A.B., PEPPER M.S., MCMAHON G.,
J. BIOL. CHEM. 271:32499-32502(1996).
SEQUENCE FROM N.A.
MEDLINE; 95211842.
LINDSELL C.E., SHARBER C.J., BOULTER
CELL 80:909-917(1995).
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GENOMICS 43:376-379(1997).
EMBL, AF003837; G2228793; -.
FOSITE, PS01187; EGF_CA, 8.
GLYCOPROTEIN: EGF-LIKE DOMAIN.
SEQUENCE 1218 AA; 133858 MW;
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05,
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Best Local Similarity 38.6%;
Matches 86; Conservative
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015122 PRELIMINA
015122;
01-JAN-1998 (TREMBLREL.
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Length 1218;

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RESULTANT AND ACCORDING TO THE PROPERTY OF THE
RESULT 12
ID 042347;
AC 042347;
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DT 01-JAN-1998 (
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OS GALLUS GALLUS
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Best Local :
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Best Local
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TISSUE-SPIAL CORD:
MYATA, HENRIQUE D., ISH-HOROWICZ D.
DEV. BIOL. 174:233-247(1996).
EMBL; X95283; E224084; -..
PROSITE; PS01010; ASX_HYDROXYL; 10.
PROSITE; PS01187; EGF_CA; 8.
GLYCOPROTEIN; EGF-LIKE DOMAIN.
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDAT
C-SERATE-1 PROTEIN (FRAGMENT).
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPO
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nes 85; Conser
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nes 86; Conser
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                                                                                                                                                                                                                                                                                  CRPRDDFFTHHTCDQNGNKTCLEGWTGPECN 204
                                                                                                                                                                                                                                                     CRPRDDSFGHSTCSETGEIICLTGWQGDYCH
                                                                                                                                                                                                                                                                                                                                                                                    NDNS-TNPDRI-IEKASHSGMINPSRQWQTLKHNTGAAHFEYQIRVTCAEHYYGFGCNKF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLALLC-ALRAKVCGASGQFELEILSMQNVNGBLQNGNCCGGARNPGDRKCTRDECDTY 74
                                                                                                                                                                                                                                                                                                                                                          NNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTCDLNYYGSGCAKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWPGTFSLIVEAWHDT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVHS-SGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCL-GSCKTRFRVCLKHYQATI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFSLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRYCLKHYQATIDTTSQCTYGDYITPILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKVCLKEYQSRVTAGGPCSFGSGSTPVIGGNTFNLKAS-RGNDR---NRIVLPFSFAWPR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLTAFICFTVIVQVH-SSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCL-GSCKTR
     GALLUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1193 AA;
                            (TREMBLREL.)
(TREMBLREL.)
(TREMBLREL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.0%;
larity 40.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.9%;
larity 38.6%;
Conservative
     (CHICKEN)
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131039 MW;
                                                      9,66
                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 587; DB 2; L
Pred. No. 9.19e-115;
52; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 573; DB 12;
Pred. No. 3.04e-111;
                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                      UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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Best Local S
Matches 6
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                            JEN W.C., WEITSTEIN D.A., CHITN SUBMITTED (DEC-1996) TO EMBL/GE EMBL; U70843; G1695891; -. PROSITE; PS01186; EGF_Z; 7. PROSITE; PS01187; EGF_CA; 2. GLYCOPROTEIN; EGF-LIKE DOMAIN. SEQUENCE 642 AA; 70667 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P79941;
P79941;
01-MAY-1997 (TREMBLREL. 03, C
01-MAY-1997 (TREMBLREL. 03, L
01-JAN-1998 (TREMBLREL. 05, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-DELTA-2.
XENOPUS LAEVIS (AFRICAN CLAWED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTCH LIGAND X-DELTA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INT. J. DEV. BIOL. 40:108: EMBL; D87558; D1022568; PROSITE; PS01187; EGF_CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
HAYASHI H., MOCHII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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NON_TER 1 1
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      179
                                                                                 120
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                                            154
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: |:|| ||:|| |:||:||:||
DTTSQCTYGDVTTPILGENSVNLTDAQRFQNKG-F--TNPIQFPESFSWPGTFSLIVEAW
                                                                                                                                                                                          SCNIFFRVCLKHAQPVVSPDPPCTFGSAVSDILPSDSKAITDS------S-PIRVPFH
                                                                                                                                                                 SCKTRFRVCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKFCRPRDDSFGHSTCSETGEIICLTGWQGDYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKFCGPRDDFVGHYTCDQNGNKACMEGWMGEEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTCDLNYYGSGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.9%;
Similarity 38.5%;
82; Conservation
                                                                                                                                                                                                                                                 Similarity 68; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1212 AA; 134188 MW;
                                                                                                                                                                                                                                                 Conservative
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X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KODAMA
                                                                                                                                                                                                                                                                                                                                                                                                                               ., CHITNIS A.B., KI EMBL/GENBANK/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 553;
Pred. No. 3.
49; Mismatc
                                                                                                                                                                                                                                              Score 516; DB 12;
Pred. No. 5.51e-97;
41; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAST SEQUENCE UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA;
                                                                                                                                                                                                                                                                                                                              2B0DDF2A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OECF076C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226
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3.16e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINTNER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DATA BANKS
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                                                                                                                                                                                                                                                 51;
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                                                                                                                                                                                                                                                                                      Length 642;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVES;
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                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G.,
                                                                                                                                                                                                                                                 Gaps
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RESULT 14 ID P97607

PRELIMINARY;

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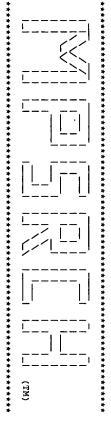
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PAGAAGDRARARSRIGGHQDPGLVVIPFQFAWPRSFILIVEAW-DWDND-ITPDEELLIE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 GPCRLFFRVCLKPGVSQEATESLCALGAALSTSVPVYTEHPGESAAALPLP-DGLVRVPF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 -TDA---Q-REQNK--GFTNP--IQFPFSFSWPGTFSLIVEAWHDTNNSGNARTNKLLIQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 RVSHAGMINPEDRWKSLHFSGHVAHLELQIRVRCDENYYSATCNKFCRPRNDFFGHYTCD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACCDGDGRTTRAGGCGRDECDTYVRVCLKEYQAKVTPTGPCSYGYGATPVLGSNSFYLP 60
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01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
1AGGEDZ (FRAGMENT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M-DELTA-LIKE 3 GENE PRECURSOR.
M-DELTA-LIKE 3.
M-DELTA-LIKE 3.
M-DELTA-LIKE 3.
EUKARYOTA- MOUSE).
EUKARYOTA- METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 485; DB 10; Length 1202;
Pred. No. 2.76e-89;
39; Mismatches 64; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 585;
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Pred. No. 8.14e-33;
41; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                         SHAWBER C.J., BOULTER J., LINDSELL C.E., WEINMASTER G.; DEV. BIOL. 180:370-376(1996).
EMBL: 970050, GJ718248; -.
PROSITE: PSO1187; EGF.CA: 7.
GLYCOPROTEIN; EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  697F4205 CRC32;
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0F5E6187 CRC32;
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Best Local Similarity 40.3%;
Matches 79; Conservative
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Best Local Similarity 25.3%;
Matches 37; Conservative
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b 170 FSYRARCEPPAVGAACARLCRSRSAP 195
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Search completed: Fri Jun 12 12:06:25 1998 Job time : 55 secs.

QY 178 YDFRVTCDLNYYGSGCAKFCRPRDDS 203



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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Jun 13 06:53:25 1998; MasPar time 3140.54 Seconds 1536.627 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-08-083-590A-1 (1-2892) from US08083590A.seq 2892

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 457396 seqs, 834342348 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database:

genbank106 1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om 7:em_or_8:em_ov 9:em_pat 10:em_pl 11:em_ro 12:em_vi

13:gb_ba 14:gb_htg 15:gb_in 16:gb_om 17:gb_ov 18:gb_pat 19:gb_ph 20:gb_pl 21:gb_prl 22:gb_pr2 23:gb_ro 24:gb_st 25:gb_sy 26:gb_un 27:gb_vi

Statistics: Mean 11.940; Variance 6.492; scale 1.839

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description | Pred. No. |
|---------------|-------|----------------|--------|-----|-----------|------------------------|-----------|
| 1 | 2892 | 100.0 | 2892 | 15 | DROEGFLEA | Drosophila sp. epiderm | 0.00e+00 |
| 2 | 2892 | 100.0 | 2892 | 18 | I56055 | Sequence 5 from patent | 0.00e+00 |
| ω | 2871 | 99.3 | 2889 | 15 | DMDELTA | D.melanogaster Dl mRNA | 0.00e+00 |
| L | 2746 | 95.0 | 4724 | 15 | DMDLG | Drosophila mRNA for De | 0.00e+00 |
| ر ن | 564 | 19.5 | 600 | 15 | DMDLEGFH | Drosophila melanogaste | 0.00e+00 |
| 6 | 169 | 5.8 | 2187 | 17 | GGU26590 | Gallus gallus C-Delta- | 3.91e-97 |
| 7 | 131 | 4.5 | 3162 | 22 | AF003522 | Homo sapiens Delta mRN | 4.31e-69 |
| œ | 115 | 4.0 | | 17 | DRDELTAD | D.rerio mRNA for Delta | 1.72e-57 |
| 9 | 111 | 3. 8 | | 23 | RNU78889 | Rattus norvegicus Delt | 1.29e-54 |
| 10 | 108 | 3.7 | | 23 | MMDELTA1 | M.musculus mRNA for De | 1.81e-52 |
| 11 | 100 | 3.5 | _ | 17 | AF006488 | Danio rerio deltaB mRN | 8.92e-47 |
| 12 | 94 | ω . ω | 2166 | 1.7 | XELXDEL | Xenopus laevis X-Delta | 1.53e-42 |
| 13 | .79 | 2.7 | 3051 | 17 | AF030031 | Danio rerio DeltaA (de | 3.92e-32 |
| c 14 | 71 | 2.5 | 7218 | 18 | 166494 | Sequence 14 from paten | 1.05e-25 |
| 15 | 70 | 2.4 | 2869 | 17 | XLU70843 | Xenopus laevis Notch l | 4.90e-26 |
| | | | | | | • | 4 |

| ď | л | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 5 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 |
|-------------------|--------------|----------|-----------|----------|----------|------------------------|----------|----------|------------------------|----------|----------|----------------|-------------------|------------|-----------|------------------------|-----------|------------------------|------------------------|------------------------|------------|----------|-----------------------|-------------|------------------------|--------|------------------------|------------------------|--------------------|------------------------|
| å | × | 50 | 50 | 51 | 51 | 51 | 51 | 51 | 51 | 53 | 51 | 51 | 51 | 52 | 51 | 56 | 54 | 54 | 54 | G G | 54 | 58 | 57 | 57 | 57 | 57 | 57 | 57 | 62 | 63 |
| ; | 1 7 | • | | ٠ | | • | | • | | • | | | | 1.8 | | | 6 | 9 | .9 | 9 | | | | O | | | | | <u>;</u> | .2 |
| i c | 25051 | 7471 | 3582 | 5942 | 5590 | 5457 | 5445 | 4974 | 4860 | 4855 | 4749 | 4702 | 4635 | 2388 | 2101 | 17137 | 8287 | 5546 | 5401 | 5274 | 1674 | 10452 | 7579 | 7332 | 5575 | 3609 | 1980 | 1483 | 7646 | 3362 |
| Ļ | 17 | 17 | 17 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 15 | 15 | 5 | 23 | 5 | 15 | 15 | 15 | 15 | 23 | 21 | 23 | 23 | 15 | 15 | 5 | 15 |
| 2004080 | AB004879 | BRNOTCH | GGCSERRAT | | HSU73936 | AF028593 | HSU77720 | AF029778 | AF029779 | HSU61276 | AF020201 | AF003521 | HSY14330 | SUEFIBRIII | SUEFIBRIA | DRONOTCH03 | RATNOTCHX | DROTMLPA | DMSLIT | DMSER | DROSLITEGE | DRONOT05 | D32210 | HUMTAN1 | RATJAPR | MMMOTB | SUSEGFIII | SUSGFE | AF000634 | SUSEGFI |
| nan tantibes Aene | nan rubrines | rio Note | _ | sapiens | | Homo sapiens transmemb | m | | Homo sapiens hJAG2.del | | | sapiens Jagged | o sapiens partial | urchin | | D.melanogaster Notch l | 7 | D.melanogaster serrate | Drosophila mRNA for sl | D.melanogaster Serrate | | | Mus musculus (Notch2) | AN-1 mRNA (| Rattus norvegicus jagg | | Strongylocentrotus pur | S.purpuratus epidermal | ytechinus variegat | Strongylocentrotus pur |
| | 370- | .33e- | φ | 1.04e-13 | 1.04e-13 | .04e- | .04e- | 1.04e-13 | .04e- | .80e- | .04e- | 1.04e-13 | .04e- | .46e- | .04e-1 | .29e- | .36e-1 | 1.36e-15 | .36e-1 | .29e- | .36e-1 | .81e- | 1.67e-17 | .67e- | .67e- | .67e- | 6 | 1.67e-17 | .69e-2 | 2.15e-21 |

ALIGNMENTS

| | mutation | | | mu ca c r On |) + + | | | | gene | | source | FEATURES | MEDLINE | JOURNAL | | | TITLE | | AUTHORS | REFERENCE | | | ORGANISM | SOURCE | | KEYWORDS | NID | ACCESSION | DEFINITION | LOCUS . | beering 1 |
|--|----------|---|-------------------------|--------------|-------------|-------------|------------|---------------|--------|--|--------|---------------------|---------|------------------------------|-------|---|---|--------------------------------------|--|---------------------|--|--|----------------|---------------------|----------------------|--|---------|-----------|------------|--------------------|-----------|
| /gene="DI" /note=""a' in mutation" /label=Dlsup4 | | /label=Dlsup5 /db xref="FlyBase:FBqn0000463" | /note="'a' in mutation" | /gene="D1" | | /allele="5" | /gene="D1" | /note="Delta" | 1 2892 | /oiganism="prosophita sp. /db_xref="taxon:7242" | 12892 | Location/Qualitiers | | Neuron 9 (5), 847-859 (1992) | vitro | Delta modify Drosophila development and affect cell adhesion in | Single amino acid substitutions in EGF-like elements of Notch and | Campos-Ortega. J. A. and Young M. W. | Lieber, T., Wesley, C.S., Alcamo, E., Hassel, B., Krane, J.F., | 1 (bases 1 to 2892) | Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Frahydroidea: Drosonhilidae: Drosonhila | Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; | Drosophila sp. | Drosophila sp. DNA. | factor-like protein. | Delta gene; Notch gene; cell adhesion activity; epidermal growth | 9290222 | L03725 | | 2892 bp DNA INV 22 | |

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0; Mismatches 0;
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strain, 'c' in variation"
/db_xref="Flybase:Fbgn0000463"
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cal Similarity 100.0%;
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| | ATCCCGAATT | 2881 | Qy |
|---------------|--|------|----|
| | GATCCCGAATTC 2892 | 2881 | ф |
| TC 2880 | ACTCGTAAACTCCCTAAAAAATTTGTATAGTAATTAGCAAAGCTGTGACCCAGCCGTTTC | 2821 | Qy |
| TC 2880 | CTCGTAAACTCCCTAAAAAATTTGTATAGTAATTAGCAAAGCTGTGACCCAGCCGT | 2821 | дb |
| A 28 | | 2761 | Qy |
| TA 2820 | TTGTTGTTGATTGAAGCAGTTTAGTCGTCACGAAAAATGAAAAATCTGTAACAGGCA | 2761 | Ф |
| AT 2760 | ACAGCACATACACAAAGAAAAGACTGGGTTGGGTTCAAAATGTGAGAGAGA | 2701 | Qy |
| AT 2760 | CAGCACATACACAAAGAAAAGACTGGGTTGGGTTCAAAATGTGAGAGAGA | 2701 | 망 |
| TG 2700 | TAACTCCAAAAATCCGGAAGGGCTCCTGGTAAATCCGGAGAAATCCGCATGGAGGAGCT | 2641 | Qy |
| TG 2700 | HACTCCAAAAATCCGGAAGGGCTCCTGGTAAATCCGGAGAAATCCGCATGGAGGAGG | 2641 | 망 |
| TG 2640 | GGCAGCGGAGCGGGCGCAACAGCAGCGATCCGTGGTCTGCGGCACTCCGCATAT | 2581 | Qy |
| TG 2640 | GCAGCGGAGCGGGGACGGCGAACAGCAGCGATCCGTGGTCTGCGGCACTCCGCATA | 2581 | 망 |
| CG 2580 | CTAATGCCTGCAGCTTCGGCAG | 2521 | Qy |
| - n | CGGCGGCGGAGTGGCCGGAGCCTGTTCATCCCAGCTAATGGCTGCAGCTTCGGCAG | 2521 | рь |
| TG 2520 | GGCAAGAGGATCTCTGTTTTAGGCGAGGGTTCCTACTGTAGCCCAGCGTTGGCCCTCGTT | 2461 | Qy |
| TG 2520 | GCAAGAGGATCTCTGTTTTAGGCGAGGGTTCCTACTGTAGCCAGCGTTGGCCCTCG | 2461 | Дb |
| AG 2460 | GTTCGCCGGCAGGCAGCTCAGCCAAGGGAGCGTCTGGCGGAGGACCGGGAGCGGCGG | 2401 | Qy |
| AG 2460 | GTTCGCCGGCAGGCAGCTCAGCCAAGGGAGCGTCTGGCGGAGGACCGGGAGCGGCGG | 2401 | DЬ |
| GC 2400 | CCGCTACAAAGAGCCAAGTCGCAAAAAGCAACTCAACACCGATCCCACGCTCATGCACCC | 2341 | Qy |
| | CGCTACAAAGACCCAAGTCGCAAAAGCAACTCAACACCGATCCCACGCTCATGCACC | 2341 | Дb |
| CT 2340 | GCGGATATGTGGCCTCGGTGGCGGATAACAACAACGCCAACTCTTTTGTGTGGC | 2281 | Qγ |
| CT 2340 | GCGGATATGTGGCCTCGGTGGCGGATAACAACAATGCCAACTCAGACTTTTGTGTG | 2281 | 망 |
| AC 2280 | TGTGCCTCAGCAGCAGCAGCGGCGGCGGCGGCAGCGACGAGCGACGA | 2221 | Qy |
| | GCCTCAGCAGCAGCAGCGGCGGCGGCGGCAGCAGCGGCGGACGAGTGTCTCATGT | 2221 | рb |
| TT 2220 | TTCGATGGCGGCAACCCGAATATCATCAAAAACACCTGGGACAAGTCGGTCAACAACAT | 2161 | Qy |
| TT 2220 | TCGATGGCGGCAACCCGAATATCATCAAAAAACACCTGGGACAAGTCGGTCAACAAC | 2161 | дg |
| CC 2160 | GGTGTAGCTTTGGCTTCAGCCTCTCTGGGCGGCAAAACTGGCAGCAACAGCGGTCTCAC | 2101 | γQ |
| CC 2160 | GTGTAGCTTTGGCTTCAGCCTCTCTGGGCGGCAAAACTGGCAGCAACAGCGGTCTC | 2101 | Дb |
| TG 2100 | GCCAGGAAGCAGAACGAACAGAATGCGGTGGCCACAATGCATCACAATGGCAGTGGGGT | 2041 | Qy |
| | CCAGGAAGCAGAACGAACAGAATGCGGTTGGCCACAATGCATCACAATGGCAGTTGGGG | 2041 | рь |
| AG 2040 | TGCGTGGTCTTCTGCATGAAGCGCAAGCGTAAGCGTGCTCAGGAAAAGGACGACGCGG | 1981 | Οу |
| AG 2040 | GCGTGGTCTTCTGCATGAAGCGCAAGCGTAAGCGTGCTCAGGAAAAGGACGACGACGCG | 1981 | В |
| CG 1980 | CAGGTAGTCCTAATTGCTGTTTTCTCCGTTGCGATGCCTTTGGTGGCGGTTATTGCGG | 1921 | Qy |
| CG 1980 | AGGTAGTCCTAATTGCTGTTTTCTCCGTTGCGATGCCTTTGGTGGCGGTTATTGCGG | 1921 | ₽ |
| CC 1920 | | 1861 | Qy |

RESULT 2

| Db 721 GC | Qy 661 AC | Db 661 AC | Qy 601 GT | Db 601 GT | 541 C | 541 CA | 481 AT | 481 | Db 421 GAG Qy 421 GAG | Qy 361 GC | Db 361 GC | 301 | 301 | 0v: 241 AG | 181 | Db 181 TT | Qy 121 GC | Db 121 GC | Qy 61 CA | Db 61 CA | Qy 1 GA | Db 1 GA | Query Match Best Local Matches 28 | BASE COUNT ORIGIN | JOURNAL FEATURES SOUICE | | | REFERENCE AUTHORS | SOURCE ORGANISM REFERENCE AUTHORS | NID KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS | ACCESSION NID KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS | DEFINITION ACCESSION NID KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS | OCUS EFFINITION CCESSION ID EYWORDS OURCE OURCE ORGANISM EFERENCE AUTHORS |
|---|-----------|--|-----------|---|--|--|--|---|---|--|--|-----|-----|---|--|--|---|--|--|--|---|---|--|----------------------|--|--|------------------------|--|---|--|--|---|---|
| CAAGTTCTGCCGGCCCCGCGACGATTCATTTGGACACTCGACTTGCTCGGAGACGGGC 78 | 72 | GCTGGAGTACGATTTCCGTGTCACCTGCGATCTCAACTACTACGGATCCC | | GGAGGTGTCCTCCGAATGGAAGACGAACAAGTCGGAATCGCAGTAC 66 | ATGATACGAACAATAGCGCAATGCGCGAACCAACAAGCTCCTCATCCAGCGACTCTTG 600 | TGATACGAACAATAGCGGCAATGCGCGAACCAACAAGCTCCTCATCCAGCGACTCTTG 600 | CCAGTTCCCCTTCTCGTTCTCATGGCCGGGTACCTTCTCGCTGATCGTCGAGGCCTGG 5 | CAGTTCCCCTTCTCGTTCTCATGGCCGGGTACCTTCTCGCTGATCGTCGAGGCCTGG 5 | AGAACTCGGTCAATCTGACCGACGCCCAGCGCTTCCAGAACAAGGGCTTCACGAATCCC 480 | GCCACCATCGACACCACCTCCCAGTGCACCTACGGGGACGTGATCACGCCCATTCTCGGC 420 | CACCATCGACACCACCTCCCAGTGCACCTACGGGGACGTGATCACGCCCATTCTCGGC 420 | | ω | AGCAACGATCACGGGCGGAACAACGAGGGTCGCTGCACCGGGGAGGTCGGACGGA | CACAGTCATCGTGCAGGTTCACAGTTCCGGCAGCTTTGAGTTGCGCCTGAAGTACTTC 2 | CACAGTCATCGTGCAGGTTCACAGTTCCGGCAGCTTTGAGTTGCGCCTGAAGTACTTC 240 | AACAAAAACATCAATAAACATGCATTGGATTAAATGTTTATTAACAGCATTCATT | GCAACAAAAACATCAATAAACATGCATTGGATTAAATGTTTAACAGCATTCATT | RACACACACACACAGCCCGTGGATTATTACACTAAAAGCGACACTCAATCCAAAAAATCA 120 | CACACACACACACACGCCCGTGGATTATTACACTAAAAGCGACACTCAATCCAAAAAAATCA 120 | GAATTCGGAGGAATTATTCAAAACATAAACACAATAAACAATTTGAGTAGTTGCCGCACA 60 | ATTCGGAGGAATTATTCAAAACATAAACACAATAAACAATTTGAGTAGTTGCCGCACA 60 | h 100.0%; Score 2892; DB 18; Length 2892; Similarity 100.0%; Pred. No. 0.00e+00; Similarity 100.0%; Pred. No. 0.00e+00; Indels 0; Gaps | 98. | Patent: US 5648464-A 5 15-JUL-1997; Location/Qualifiers 12892 //rapitsm="unbown" | inding domains in toporythmic proteins | Blaumueller, C. Marie. | 1 (bases 1 to 2892) Artavanis-Tsakonas,S., Fehon,R.Grant, Rebay,I. and | fied. s 1 to 2892) s-Tsakonas,S., Fehon,R.Grant, Rebay,I. a | ehon,R.Grant, Rebay,I. a | Pehon,R.Grant, Rebay,I. a | JS 5648464. | DNA PAT JS 5648464. |
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|------------|---|---|--------|--|--------|-----------|---|--------|--|--------|--|--------|------------------|--------|--------|--------|--|--------|--|-------------------------|---|--------|---|--------|---------|--------|--|--------|---------------|--------|---|--|
| 1801 | 1861 | 1921 | 1981 | 1981 | 2041 | 2041 | 2101 | 2161 | 2161 | 2221 | 2221 | 2281 | 2281 | 2341 | 2341 | 2401 | 24.0 | 2401 | a+ ⊓ | 2521 | 7.02 | n L | 708 | 2641 | 2641 | 7/07 | 2701 | 2761 | 276 | 2821 | 2881 | 2881 |
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| 780 | 840 | 90 | 6 | 096 | | 1020 | 108 | 108 | 1140 | 120 | 12 | 1260 | 12 | 1320 | 13 | 1380 | 1380 | 1440 | 1440 | 1500 | c 1500 | 1560 | 1560 | 1620 | 1620 | 1680 | 168 | 1740 | 1740 | 1800 | 1800 | 1860 |
| ACGGGC | GCCAAA | TGGAAG | TGGAAG | AACAAP | CTGAAC | CTGAAC | GAGGGA | GAGGG | ATCTAC HILLI | CCGCAC | CCCCAC | GAGGAG | | | CGTCCT | GGACCC | GGACCC | AGCTG | AGCTGT | CA | - 8 | GTCAAC | GTCAAC | GTTGAC | GTTGAC | GATTAC | GATTAC | GAGTG | GAGTGC | GAATG | GAATG | GTGACC |
| | AATGC | TGGGC | TGGGC | SCACCTGCAACAAA | AGGAT | AGGAT | 11111 | 00000 | ATGAG | ATGAG | ATGAG | ATGTGC | I I I I I I | ACGTT | AACGTT | PACAGO | racago | SGTGGA | GTGGA | recease | rgcgagag | SATATG | SATATG | AGCAAA | AGCAAA | AACAAC | AACAAC | ATCGAT | ATCGAT | rcgrrc | CGTTC | SATTCG |
| | GAAATTATCTGTTTGACCGGATGGCGGGTTACTGTCACATACCCAAATGCG | GAACATGGACATGCGACAAACCCAATGCGTTTGCCAACTGGGCTGGAAG | GCCAAC | ATGGCA | GCAACO | | TACTGCACCAACCACACACCCTGCAAGAATGGCGGAACCTGCTTCAACACCGGCC | TCAAC | TTGTRCACACATCCAATGCGCTCCAGGATRCAGTGGTGATCATTGCCAAATGAGATCTTC | GCATC | GCCGATGTCAATCCCTGCCAGAATGGTGGTACCTGCATCGATGACGCCGCAC | GAAAG | | 709009 | | TTGGC | GCTTGGGAAGGAAGGGTCAGGGCTACCAGTGCGAATGTCCCATTGGCTACAGGGACCC | TAAACC | CTCCAGCTGGACAACTGCAGTCCGAATCCATGCATAAACGGTGGAA | CGAGA | CAGCCGAGCGGAAAGTGTATTGCCCAGCGGGATTTTCGGGAACGAGT | GCATAC | CTTGGCCACCAGGGGGAGGCACCTGCATAGATATGGTCAAC | GTAGT | | ATCTC! | GTGCCAATGGAGGAACCTGCTTGAATCTCAACAACGATAC | TGGAC | | TCAAT | GGACCCTGTCATAACGGCGGCACTTGCATGAACCGCGTCAATTCGTTCG | GTGTGTGCCAATGGTTTCAGGGGCAAGCAGTGCGATGAGGAGTCCTACGATTCGGTGACC |
| | STCACA | SCGTTT | CGTTT | CCTTGTGCAACGAGTGCGTTCTGGAACCGAACTGCATCCATGG [| GTACT | GTACT | CTGCT | CTGCT | ATGATT | TACCT | TACCT | SGAGCG | IIIIII 3GAGCG | SAATCT | SAATCT | STCCCA | STCCCA | CATGCA | CATGCA | CGGGAA | GGGAA | SCACCT | SCACCT | CCACT | CCACT | SCTTGA | SCTTGA | SCICIG | SCICIG | ACCGCG | ACCGCG | AGGAGT |
| TGGACA | TTACTO | TCAATG | TCAAT | GAACTC | AGGCT | AGGCTJ | CGGAAC | CGGAAC | 166167 | TGGTGC | TGGTGC | CGGCTC | CGGCTC | TCAGG | TCAGG | CGAATC | CGAATC | GAATCC | GAATC | ATTTT | ATTTT | CGGAGG | CGGAG | TGGCAC | TGGCAC | AACCT(| AACCTC | GGATT | GGATT | CATGA | CATGA | CGATG |
| | 366CGA | CCCAA | cccaa | GAACC | TGGGG | 11111 | SAATGG | PAATGG | ATACAG | CAGAA | CAGAA | GCCAA | GCCAA | TGTCA | TGTCA | CAGTG | CAGTG | CAGTCC | CAGTCC | 4GCGGG | AGCGGG | GAGAA | GAGAA | TTCCA | FITCCA | rggagg | FGGAGG | IGGCAA | I I I I I I I | CACTTG | CACTIG | SCAGIG |
| SACGAT | rggcag | SACAAA | SACAAA | STTCTG | 3AGGG1 | | rgcaag [| FGCAAG | | CCTGC | CCTGC | CATTGC | CATTGC | AAACCC | AAACCO | GGCTAC | GCTAC | AACTGC | AACTGC | TGCCC2 | TGCCC# | CAGTGC | CAGTGC | 55555 | | GCCAA1 | GCCAA3 | TTTAC | TTTAC | 20000 | 099999 | GGCAAC |
| 1111 | CCGGA | ATTGC | ATTGC | AGTGC AGTGC | GCAAC | GCAAC | GACCC | GACCC | | TCAAT | TCAAT | AGTGT | AGTGT | CGGAC | CGGAC | GTCAG | GTCAG | TGGAC | TGGAC | GTATT | GTATT | GCCAC | CCAC | GCGTT | GCGTT | CGTGT | CGTGT | CGGGA | CGGGA | ATAAC | ATAAC | TCAGG |
| 255225 | TITGA | VTGGAC | VTGGAC | SCAACG | CATCT | SCATCT | CCACA | CCACA | CAAAT | CGATG | CGATG | SCIACA | SCTACA | GTGTT | CTCTT | SCAAGG | SCAAGG | CCAGC | rccago | SAAAGT | SAAAGT | TCTTG | STCTTG | SCCAAT | CCAAT | CAGAC | CTCATCAGACCGTG | STCGTG | STCGTG | CCTGTC | CTGTC | ATGGTT |
| STTCTG | TATCTG | GAACA | GAACA | TTGTG | SACTIC | SACTION | SACCAR | ACCA | ACATO | GATG | GATG | AACCGC | AACCGG | SCTCAC | SCTCAC | GGGAAG | GGGAAC | GGATC | GATC | SAGCGC | SAGCGC | CGATTC | CGATTC | TCGCTC | rcccrc | CCTCA | CCTCA | CACCTO | CACCTC | TGGACC | TGGAC | TGCCA/ |
| GCCAAGT | GAAATI GAAATI | GGCTGTC | GGCTG | GGAGC | CCCTG | cccrg | TACTG | TACTG | TTGTAC | TCCTG | TCCTGCGATG | ACAAA | ACANA | AAAGT | | GGCTT | GGCTT | AACTG | AACTGCGATC | CAGCC | CAGCC | ATTGA | ATTGACGATTGTC | CAATA | CAATATO | TTGTG | TTGTGCC | CAGTG | CAGTG | AGCAG | AGCAGIG | GTGTG |
| 721 | 781 | 41 | | 901 | | 961 | | | 1081 | | | | | 1261 | 61 | 1321 | 1321 | 1381 | 1381 | 1441 | 1441 | 1501 | 1501 | 1561 | 1561 | 1621 | 21 | 1681 | 1681 | 1741 | 1741 | 1801 |
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TGTGCCAATGGTTTCAGGGGCAAGCAGTGCGATGAGGAGTCCTACGATTCGGTGACC 1860 AGGAACCAGAACAGAATGCGGTGGCCACAATGCATAACAATGCAGTGGGGTG AAGAGGATCTCTGTTTTAGGCGAGGTTCCTACTGTAGCGGCGGCGTTGGCCCTCGTTG CAGCGGAGCGGGACGGCGCAACAGCAGCGATCCGTGGTCTGCGGCACTCCGCATATG GTGGTCTTCTGCATGAAGCGCAAGCGTAAGCGTGCTCAGGAAAAGGACGACGCGGAG CTACAAAGAGCCAAGTCGCAAAAGCAACTCAACACCGATCCCACGCTCATGCACCGC TTCGCCGGCAGGCAGCTCAGCCAAGGGAGCGTCTGGCGGAGGAACGGGAGCGGCGGAG GATGCCCACCAATATGGAGCGACCACACAAGCGAGAGCCGATGGTTTGACCAATGCC GTAGTCCTAATTGCTGTTTTCTCCGTTGCGATGCCTTTGGTGGCGGTTATTGCGGCCG GATCCCGAATTC 2892 CCCGAATTC 2892

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Submitted (14-JUN-1991) M.A.T. Muskavitch,
Indiana University, Bloomington, Jordan Hai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="plD:g577774"
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/db_xref="FlyBase:FBgn0000463"
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| | 1 CCCTGGACTTGCATCTGCAAGGGTTGGGGAGGCTTGTACTGCAACCAGGATCTGAAC | 1 TACTGCACCAACCACAGACCTGCAAGAATGGCGGAACCTGCTTCAACACCGGCGAGGGA | 1 TTGTACACATGCAAATGCGCTCCAGGATACAGTGGTGATGATTGCGAAAATGAGTCTAC | 1 TCCTGCGATGCCGATGTCAATCCCTGCCAGAATGGTGGTACCTGCATGAGGCGGCAC | 01 ACAAAAACCGGCTACAAGTGTCATTGCGCCAACGGCTGGAGCGGAAAGATGTGCGAGGAG 11 | 1 AAAGTGCTCACGTGTTCGGACAAACCCTGTCATCAGGGAATCTGCCGCAACGTTCGTCCT | 21 GGCTTGGGAAGCAAGGGTCAGGCTACCAGTGCGAATGTCCCATTGGCTACAGCGGACCC | 81 AACTGCGAICTCCAGCTGGACAACTGCAGTCCGAATCCATGCATAAACGGTGGAAGCTGT | 1 CAGCCGAGCGGAAAGTGTATTTGCCCAGCGGATTTTCGGGAACGAGATGCGAGACCAAC | 01 ATTGACGATTGTCTTGGCCACCAGTGCGAGACGGAGCACCTGCATAGATATGGTCAACCCACCACTGCATTGTTTTTTTT | 61 CAATATGGCTGCCAATGCGTTCCCGGTTTCCATGGCACCCACTGTAGTAGCAAAGTTGAC | 1 TIGTGCCTCATCAGACCGIGTGCCAATGGAGGAACCTGCTTGAATCTCAACAACGATTAC | 81 CAGTGCACCTGTGGGGGATTTACTGGCAAGGATTGCTCTGTGGACATCGATGGTGC | 41 AGCAGTGGACCCTGTCATAACGGCGGCACTTGCATGAACCGCGTCAATTCGTTCG | 01 GTGTGTGCCAATGGTTTCAGGGCAAGCAGTGCGATGAGGAGTCCTACGATTCGGTGACC | 61 TTCGATGCCCACCAATATGGAGCGACCACACAAGCGAGAGCCGATGGTTTGACCAATGC | 21 CAGGTAGTCCTAATTGCTGTTTTCTCCGTTGCAATGCCTTTGGTGGCGGTTATTGCGGCG | 81 TGCGTGGTCTTCTGCATGAAGCGCAAGCGTAAGCGTCGTCAGGAAAAGGACGCGGAG |
| 90 | 96 | 102 | 108 | 114 | 120 | 126 | 132 | 138 | 144 | 15(| 156 | 162 | 168 | 174 | 18(| 186 | 193 | 198 |
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DMDLG 4724 bp RNA INV 02-FEB-1995 DG 28050phila mRNA for Delta (D1) gene. X06289 9785. D1 gene; glycoprotein; neurogenesis; transmembrane protein. fruit fly. Drosophila melanogaster Drosophila melanogaster Eukaryotee; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; 1981 TGCGFGGFCTTCTGCATGAAGCGCAAGCGTAAGCGTGCTCAGGAAAAGGACGACGCGGAG 2040 2041 GCCAGGAAGCAGAACGAACAGAATGCGGTGGCCACAATGCATCACAATGGCAGTGGGGTG GCGGCGGCGGAGTGGCCGGAGCCTGTTCATCCCAGCTAATGGCTGCAGCTTCGGCAGCG GGCA-CGGA-CGGG-ACGGCGCAACAGCAGCGATCCGTGGTCTGCGGCACTCCGCATATG GITGITGITGAITGAAGCAGITTAGICGICACGAAAAAIGAAAAAICTGIAACAGGCAIA GGTGTAGCTTTGGCTTCAGCCTCTCTGGGCGCCAAAACTGGCAGCAACAGCGGTCTCACC GGTTCGCCGGCAGGCAGCTCAGCCAAGGGAGCGTCTGGCGGAGGGACCGGGAGCGGCGGAG GGCAAGAGGATCTCTGTTTTAGGCGAGGGTTCCTACTGTAGCCAGCGTTGGCCCTCGTTG GCCAGGAAGCAGAACAGAATGCGGTGGCCACAATGCATCACAATGGCAGTGGGGTG GGCGGATATGTGGCCTCGGTGGCGGATAACAACAATGCCAACTCAGACTTTTGTGTGGCT CCGCTACAAAGAGCCAAGTCGCAAAAGCAACTCAACACCGGTCCCACGCTCATGCACCGC GATCCCGAATIC 2889 OCUS EFINITION CCESSION ID EYWORDS OURCE ORGANISM SULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein with EGF-like repeats
EMBO J. 6, 3431-3440 (1987)
include x05140 (refering to the authors); some differences found.
Location/Qualifiers
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The neurogenic Gene Delta of Drosophila melanogaster is expressed in neurogenic territories and encodes a putative transmembrane
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/db_xref-"FlyBase:FBgn0000463"
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TKKRLGWVQNVRETPKMLLLIEAV"
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TGWQGDYCHIPKCAKGCEHGHCDKPNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWT
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                                                                                                                      Score 2746; DB 15; Length 4724; Pred. No. 0.00e+00; 0; Mismatches 35; Indels 8;
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1141 GTCAATCCCTGCCAGAATGGTGGTACCTGCATCGATGAGCCGCACACAAAAACCCGGCTAC 1200
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| AAACCGGCTAC 1200 | ををきしました プランジング ひょうしゅう プラム・プライン はいじょうじゅん マンタン プランシー マイン・アン・ファン・ファン・ファン・ファン・ファン・ファン・ファン・ファン・ファン・ファ | 1141 | 3 | |
|------------------|--|------|----------|--|
| GCGATGCCGAT 1155 | TGCGCTCCAGGATACAGTGGTGATGATTGCGAAAATGAGATCTACTCCTG | 1096 | Qy | |
| CGATGCCGA | GCGCTCCAGGATACAGTGGTGATGATTGCGAAAATGAGATCTACTCCTG | 1081 | ф | |
| ACACATGCAAA 1095 | AGACCCTGCAAGAATGGCGGAACCTGCTTCAACACCGGCGAGGGATTGTA | 1036 | Оу | |
| ACACATGCA | GACCCTGCAAGAATGGCGGAACCTGCTTCAACACCGGCGAGGGATTGT | 1021 | Db | |
| CACCAAC | TGCAACGAGGGTTGGGGAGGCTTGTACTGCAACCAGGATCTGAACTACTG | 976 | Qy | |
| CACCAACC | GCAACGAGGGATGGGGAGGCTTGTACTGCAACCAGGATTTGAACTAC | 961 | дд | |
| | GAGTGCGTTCTGGAACCGAACTGCATCCATGGCACCTGCAACAAACCCTG | 916 | Qy | |
| GGACTTGCATC 960 | GAGTGCGTTCTGGAACCGAACTGCATCCATGGCACCTGCAACAAACCCTGGACTTG | 901 | מם | |
| CTTGTG | CATTGCGACAAACCCAATCAATGCGTTTGCCAACTGGGCTGGAAGGGAGC | 856 | ΩУ | |
| CTTGTGC | ATTGCGACAAGCCCAATCAATGCGTTTGCCAACTGGGCTGGAAAGGAGG | 841 | ДĎ | |
| ഹ – | ACCGGATGGCAGGGCGATTACTGTCACATACCCAAATGCGCCAAAGGCTGTGAACATG | 796 | Qy | |
| GTGAACATGGA 840 | ACCGGATGGCAGGGCGATTACTGTCACATACCCAAATGCGCCAAAGGCTG | 781 | дд | |
| TTATCTGTTTG 795 | CCCCGCGACGATTCATTTGGACACTCGACTTGCTCGGAGACGGGCGAAATT | 736 | Оу | |
| TTATCTGTTTG 780 | CCCCGCGACGATTCATTTGGACACTCGACTTGCTCGGAGACGGCGAAAT | 721 | ф | |
| AGTTCTGCCGG 735 | GATTTCCGTGTCACCTGCGATCTCAACTACTACTGCGATCCGGCTGTGCCAAGTT | 676 | Qy | |
| CTGCC | ATTTCCGTGTCACCTGCGATCTCAACTACTACGGAT | 661 | Db | |
| CGCTGGAGTAC 675 | GAGGTGTCCTCCGAATGGAAGACGAACAAGTCGGAATCGCAGTACACGTCC | 616 | Оу | |
| CTGGAGT | AAGTGTCCTCCGAATGGAAGACGAACAAGTCGGAATCGCA | 601 | дд | |
| AGCAGGTACTG 615 | AGCGGCAATGCGCGAACCAACAAGCTCCTCATCCAGCGACTCTTGGTGCA | 556 | Оу | |
| AGCAGGTACT | GCGGCAATGCGCGAACCAACAAGCTCCTCATCCAGCGACTCTTGGTGC | 541 | ФФ | |
| ATACGAACAAT 555 | TCGTTCTCATGGCCGGGTACCTTCTCGCTGATCGTCGAGGCCTGGCATGATAC | 496 | Qy | |
| G - | CGTTCTCATGGCCGGGTACCTTCTCG | 481 | dα | |
| TCCCCTT | CTGACCGACGCCCAGCGCTTCCAGAACAAGGGCTTCACGAATCCCATCCAG | 436 | Qy | |
| TCCCC | GACCGACGCCCAGCGCTTCCAGAACAAGGGCTTCACGAAT(| 421 | gg gg | |
| ACTCGGTCAAT 435 | ACCTCCCAGTGCACCTACGGGGACGTGATCACGCCCATTCTCGGGGAAACTCGGTCAAT | 376 | Qy | |
| ACTCGGTCAAT 420 | : 3 | 361 | σd | |
| CCATCGACACC 375 | GCAGCTGCAAGACGCGGTTTCGCGTCTGCCTAAAGCACTACCAGGCCAC | 316 | Оу | |
| CATCGACAC | GCAGCTGCAAGACGCGGTTTCGGCTCTGCCTAAAGCACTACCAGGCCA | 301 | מם | |
| GCAAGTGCCTG 315 | CGGGACAACGAGGGTCGCTGCTGCAGCGGGGAAGTCGGACGGA | 256 | Qy | |
| GCAAGTGCCTG 300 | - 6 | 241 | ф | |
| TCACGG | CAGGTTCACAGTTCCGGCAGCTTTGAGTTGCGCCTGAAGTACTTCAGCAACGA | 196 | Оу | |
| TCATG | CAGGTTCACAGTTCCGGCAGCTTTGAGTTGCGCCCTGAAGTACTTCAGCAA | 181 | Db | |
| CAGTCATCGTG 195 | ATAAACATGCATTGGATTAAATGTTTATTAACAGCATTCATT | 136 | Qy | |
| CATCGT | AAACATGCATTGGATTAACTGTTTATTAACAGCATTCAT | 121 | ДĎ | |
| CAAAAACATCA 135 | CCCGTGGATTATTACACTAAAAGCGACACTCAATCCAAAAAATCAGCAAC | 76 | Qy | |

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Drosophila melanogaster

Brusyckets, mitochondrial eukaryotes; Metazoa; Arthropoda;

Brusryckete, mitochondrial eukaryotes; Metazoa; Arthropoda;

Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 600)

Knust,E., Dietrich,U., Tepass,U., Bremer,K.A., Weigel,D., Vassin and Campos-Ortega,J.A.

EGF homologous sequences encoded in the genome of Drosophila enalonogaster, and their relation to neurogenic genes

EMBO J. 6 (3), 761-766 (1987)
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Dl locus with EGF-like
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Gallus gallus (
U26590
g882411
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l Similarity 97.0%;
582; Conservative
Gallus gallus
Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Archosauria; Aves; Neognathae; Gall
Phasianidae; Phasianinae; Gallus.
                                                                                                   chicken.
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/db_xref="swiss-prot:p10041"
/translation="cspecific record re
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/db_xref="FlyBase:FBgn0000463"
<1. .>600
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/db_xref="PID:g929563"
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s C-Delta-1
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Pred. No. 0.00e+00;
0; Mismatches 18
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    CTGACCGACCCCAGCGCTTCCAGAACAAGGGCTTCACGAATCCCATCCAGTTCCCCTTC
                       GTCCCCGACGGCGGGCGCGCCGACCCCGCTTCAGCAACCCCATCCGCTTCCCCTTC
                                                                                                        GAGCCGCCCTGCACCTACGGCAGCGCCCATCACCCCCGTCCTCCGGCGCCAACTCCTTCAGC
                                                                                                                                                                                     TGCGACTGCAAGACCTTCTTCCGCGTCTGCCTGAAGCACTACCAGGCCAGCGTCTCCCCCC
                                                                                                                                                                                                                                                                                           CTGCTCAGCAACCGCAACTGCTGCCGGGGGGGGGGGCGCCCGGAGCGCGGCAGCAGCAG
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                                                                                                                                                                      GGCAGCTGCAAGACGCGGTTTCGCGTCTGCCTAAAAGCACTACCAGGCCACCATCGACACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-MAY-1995) Domingos Henrique, Dev. Genetics
Laboratory, Dev. Biol. Unit, Imperial Cancer Research Fund, South
Parks Road, Oxford OX1 3PS, UK
Location/Qualifiers
1. 2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Henrique, D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expression of a Delta homologue in prospective neurons in Nature 375 (6534), 787-790 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Henrique, D., Ad. Ish-Horowicz, D.
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Similarity 61.1%;
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CNPGWKGQYCTEPICLPGCDEQHGFCDKPGECKCRVGWGGKYCDECIRYPGCLHGTCQ
DPWCNCQEGWGGLFCNDLNCTHHKDCKNALTCTNTGGGSTTCSCRRGYTGSSCEI
EINECDANPCKNGGSCTDLENSYSCTCPFGFYGKNCELSAMTCADGPCFNGGRCTDNP
DGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQCVDLGNSYIOCQQAGFTGHKDDN
VDDCASFPCVNGGTCQDGVNDYSCTCPPGYNGKNCSTPYSRCEHNPCHNGATCHERSN
RYVCECARGYGGLNCQFFLLPEPPGGPVIVDFTERYTEGQNSQFFWIAVCAGIILVLML
LLGCAAIVVCVELKVQKRHHQPEACRSETETMNNLANCQREKDISISVIGATQIKNTN
KKYDFHSDNSDKNGYKVAYPSVDYNLYHELKNEDSVKEEHGKCEAKCETYDSEAEEKS
AVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKDECIIATEV*
a 657 c 625 g 401 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNR
NCCRGGGPGGAGQQQCDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPD
GAGGADPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="stage 4-6, (1 day old)"
/tissue_type="spinal cord"
/clone_lib="E2 chick embryo library
Columbia University"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="C-Delta-1"
/db_xref="PID:g882412"
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/db_xref="taxon:9031"
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Pred. No. 3.91e-97;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 367;
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Artavanis-Tsakonas, S.
Direct Submission
Submitted (09-MAY-1997) Howard Hughes Medical Institute, Yale
University, 295 Congress Ave, New Haven, CT 06510, USA
                                 GACGACCTCACCACAGAAAACCCCGAGCGCCTCATCAGCCGCCTGGCCACCCAGAGGCAC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-1997
                                                                                                                                                                                                                                                                 613 CTGGAGGTGTCCTCCGAATGGAAGACGAACAAGTCGGAATCGCAGTACACGTCGCTGGAG
                                                                                                                       538 TACTCCTATCGCTTTGTGTGTGATGAGCACTACTACGGGGAAGGCTGCTCTGTCTTCTGC
                                                                                                                                                                  CGGCCCCGTGACGACCGCTTCGGTCACTTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGC
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                                                                                                                                    AATAGCGGCAATGCGCGAACCAACAAGCTCCTCATCCAGCGACTCTTGGTGCAGCAGGTA
                                                                             CTGGCGGTGGGCGAGTGGTCCCAGGACCTGCACAGCAGCGGCCGCACCGACCTCAAG
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordat
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini;
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/organism="Homo sapiens"
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Mann, R.S., Gray, G.E.,
Artavanis-Tsakonas, S.
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CPVGYSGFNCDFKIDYCSSSPCSNGAKCYDLGADYLCRCQAGFSGHCDDNYDDCASS
PCANGGTCDGVNDPSCTCPPGYTGNCSAPVSRCEHAPCHNGATCHERGHGYVCCA
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VCVRLRLQKHRPPADDFCRGFETMNNLANCQREKDISVSIIGATQIKNTKKADFHGD
HSADKNGFRARY PAUDYNLYODLKGDDTAVNDAHSKRDTKCOPQGSSGEEKGTPTTLR
GGEASERRRPDSGCSTSKDFKYQSYYYISEENDECVIATEV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 131; DB 22; Length 3162;
Pred. No. 4.31e-69;
0; Mismatches 305; Indels 13;
                                             Notch receptor"
/db_xref="taxon:9606'
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/codon_start=1
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Best Local Similarity 65.1%;
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    GCTGGAGTACGATTTCCGTGTCACCTGCGATCTCAACTACTACGGATCCGGCTGTGCCAA 725
                                       GCTGAAGTACTCATACAGATTCGTTTGTGATGAGCATTACTACGGCGAGGGCCTGCTCGGT 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Ortega, J.A. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dornseifer, P., Takke, C. and Campos-Ortega, J.A. Overexpression of a zebrafish homologue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; Metazoa; Chordata; Vertebrata; Actinopterygii; Meopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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                                                                                 Conservative
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GWGGLFCNQDLNYCTHHKPCQNGATCTNTGQGSYTCSCRPGFTGDSCEIEVNECSGSP
GRNGGSCTDLENTYSCTCPPGFTGRNCELSAMTCADGPCFNGGKADNPEGGYFCQCP
MGYAGFNCEKKIDHCSSNPCSNDAQCLDLVDSYLCQCPEGFTGTHCEDNIDECATYPC
QNGGTCQDGLSDYTCTPGYTGKNCTSAVNKCLHNPCHNGATCHEMDNRYCCAIPG
YGGRNCQFLLPENPQGQAIVEGADKRYSYEEDDGGFPWTAVCAGIILVLLVLIGGSVF
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TNPIPFAFGFTWPGTFSLIIEALHTDSTDDLSTENPDRLISRMTTQRHLTVGEBWSQD
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SSERKRTESLCKDTKYQSVFVLSEEKDECIIATEV"
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/db_xref="taxon:7955"
                                                                                                                                                                                                                          gene-"deltaD"
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                                                                                                  Score 115; DB 17; Pred. No. 1.72e-57;
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Disibio,G., Hebshi,L., Boulter,J. and Weinmaster,CDNA sequence of R. norvegicus (rat) Deltal unpublished
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Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
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U78889
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Medicine, 10833 LeConte
                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                               Disibio,G.,
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                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
/db_xref="taxon:10116"
290. .2434
                                                                   CRGGSGPPCACRTFFRVCLKHYQASVSPEPPCTYGSAVTAVLGVDSFSLPDGAGIDPA
FSNPIREPFGFTWPGTFSLIIEALHTDSPDDLATENPERLISKLTTQRHLTVGEEWSQ
DLHSGGRTDLRYSYRRPCDEHYYGEGCSVFCTRFRDDAFGHFTCGERGEKGCDPGWRGQ
YCTDPICLPGCDDQHGYCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQ
                EGWGGLFCNQDLNYCTHHKPCRNGATCTNTGQGSYTCSCRPGYTGANCELEVDECAPS PCRNGGSCTDLEDSYSCTCPPGFYGKVCELSAMTCADGPCFNGGRCSDNPDGGYTCHC PAGFSGFNCEKKIDLCSSSPCSNGAKCVDLGNSYLCRCQTGFSGRYCEDNVDDCASSP
CANGGTCRDSVNDFSCTCPPGYTGRNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQ
                                                                                                                                          /db_xref="PID:91699046"
/translation="MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNC
                                                                                                                                                                              /product="Deltal"
                                                                                                                                                                                              /codon_start=
                                                                                                                                                                                                                   /note="DSL ligand"
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Deltal mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                 Boulter, J. and Weinmaster, G
                                                                                                                                                                                                                                                                                                                                               Biological Chemistry, UCLA School of Avenue, CHS 33-257, Los Angeles, CA
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GYGGANCQFILPEPPPDLIVAAQGGSFPWVAVCAGVVLVLLLLGCAAVVVCYRLKLQ
KAQPPPDPCGEFFTWNLANCQREKDVSVSIIGATQIKNTNKKADFHGDHGADKSSF
KAYPTVDYNLIRDLKGDEATVRDAHSKRDTKCQSQGSVGEEKSTSTLRGGEVPDRKR
PESYYSTSKDTKYSVYVLSARENDEVIATEV*
788 c 806 g 569 t
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 951 CTGACCCCATTTGTCTGCCAGGCTGTGATGACCAACATGGATATTGTGACAAACCGGGGG 1010
                                                                                                                                                                                                                                                                                                                                                                                                     1011 AATGCAAGTGCAGAGTTGGCTGGCAGGGCCGCTACTGCGATGAATGCATCCGATACCCAG 1070
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                                                                                                                                                                                                                                                                                701 ACTACTACGGATCCGGCTGTGCCAAGTTCTGCCGGCCCCGCGACGATTCATTTGGACACT 760
                                                                                                                                                                                                                                                              831 ACTACTATGGAGAAGGCTGCTCCGTGTTCTGCCGACCGCGGGATGATGCCTTTGGCCACT 890
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Carl-von-Linnee-Weg 10, 50829 Koeln, FRG
revised by author 11-MAY-95
                                                                                                                                                            Gaps
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Bettenhausen, B., de Angelis, M.H., Simon, D., Guenet, J.L. and
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                                                                                                                                                          9;
                                                                                                                        Length 2795;
                                                                                                                        Score 111; DB 23; Length 279
Pred. No. 1.29e-54;
0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.musculus mRNA for Delta-like 1 protein. x80903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="17"
/map="8.5 (EUCIB resource)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Balb/c x c57BL/6"
/db_xref="taxon:10090"
/dev_stage="d 10.5 p.c."
/clone_lib="lambda ZAP II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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Bettenhausen, B.
                                                                                                                        Query Match 3.8%;
Best Local Similarity 67.0%;
Matches 278; Conservative
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house mouse.
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AUTHORS
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FSNPT REPERCETWECTES. LIEALHIDSPDDLATENBERLISBLITORHLITGEBARGE
FSNPTREPERCETWECTES. LIEALHIDSPDDLATENBERLISBLITORHLITGEBARGE
DLHSGRIDLRYSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQ
YCTDP ICLEGCDDDHGYCDRFGECKRVGMGRYCDEC IRYPGCLHGTCQDPMCCNCQ
EGWGGLFCNODLNYCTHHRPCRNGATCTHGGGSYTCSCRPGYTGANCELEVDECAPS
PCKNGASCTDLEDSFSCTPPGFYGRVCELSAMTCANGFORPGYTGANCELEVDBCAPS
PCKNGASCTDLEDSFSCTPPGFYGRVCELSAMTCANGFORPGYTGHGGOTTCHC
PLGFSGFNCERKMDLCGSSPCSNGAKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSP
CANGGTCRDSVNDSSCTPPGFYTGRNCSAPVSRCEHAPCHNGAFTCHGGGGYTCHC
GYGGPNCQFLLDEPPPGFGYTGRNCSAPVSRCEHAPCHNGAFTCHGGGYWWECAQ
GYGGPNCQFLLDEPPPGGGFFTTMNNLANCOREKDVSVSIIGATUNKAADFHGD
HGARKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSKRDTKCQSGSSAGEEKIAPTLRG
GEIPPRRRESSVYSTSKDTKXQSVYVLSAEKNDFCVIATEV"
                                                                                                                                                                                                                        /translation="MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNC
CRGGSGPPCACRTFFRVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 TGAIGGCGCAGGCAIC -- GACCCCGC-CTICAGCAACCCCAICCGAIICCCCTICGGCII 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCTGGCCAGGTACCTTCTCTGATCATTGAAGCCCTCCATACAGACTCTCCCGATGA 411
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/gene="pll1"
674. .1564
/rpt_family="EGF-like"
/rpt_unit=774. .769
/rpt_unit=770. .871
/rpt_unit=772. .991
/rpt_unit=872. .991
/rpt_unit=1106. .1122
/rpt_unit=1106. .1122
/rpt_unit=1123. .1336
/rpt_unit=1133. .1356
                                                                                                                                                               /product="DELTA-like 1"
/db_xref="PID:9806570"
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                                                                                                                                          /codon_start=1
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/gene="Dlll"
14. .210^
                                                                                                         /gene="Dlll"
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Best Local Similarity 61.6%;
Matches 498; Conservative
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RESULT 11
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Danio rerio
AF006488
g2772824
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Lobases 1 to 3007)
                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-JUN-1997) Vertebrate Development Lab, Research Fund, 44 Lincoln's Inn Fields, London WC2A
                                                                                                                                                                                                                                                                                                                                                                                                                                               pevelopment 125 (3),
98165391
                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multiple delta genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                   bases 1 to 3007)
                                                                                                                     /note-"transmembrane protein with 8 EGF-like repeats in its extracellular region; similar to Drosophila Delta protein, encoded by GenBank Accession Number 700222, Mus musculus Delta-like 1 protein, encoded by GenBank Accession Number x80903, Xenopus laevis X-Delta-1 gene, encoded by GenBank Accession Number L42229, and Chick C-Delta-1 gene, encoded by GenBank Accession Number
                                  /product="deltab"
/db_xref="PID:92772825"
/translation="MAHLSLYCLLSVSLLQLVASSGVFELKVHSFSTTRRFCRRTRDC
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NIFFRICLKHSEDVISAEPPCTFGTGGTSVLRADQSSIASSAALRVPFHFKWPGTFSL
            IIEAWNAESPKEHHDYTENQNNLISRLATRRRLAVGEDWSQDVHFGDQSELRYSYHVF
CDEFYFGEACSDYCRPRDDTLGHYTCDENGNKECLVGWQGDYCSDPICSSDCSERHGY
CESPGECKCRLGWQGPSCSECVHYPGCLHGTCSQPWQCVCKEGWGGLFCNQDLNYCTN
                                                                                                                                                                                                                                      /gene="deltaB"
191. .2038
                                                                                             /codon_start=
                                                                                                                                                                                                                       /gene="deltaB"
                                                                                                                                                                                                                                                                                                      /dev_stage="20-28 hour"
                                                                                                                                                                                                                                                                                                                        /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                           clone_lib="from
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683 TACTTCGGCGAGGCTTGTTCAGATTACTGCCGTCCTCGTGACGACACGCTTGGCCACTAT 742
                      CTCTTCTGTAACCAGGACCTCAACTACTGTACCAATCACAAACCCTGCGCTAATGGCGCC
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ACCTGCTTCAACACCGGCGAGGGATTGTACACATGCAAATGCGCTCCAGGAT
                                                                                             TTGTACTGCAACCAGGATCTGAACTACTGCACCAACCACAGACCCTGCAAGAATGGCGGA
                                                                                                                                                                                          TGCATCCATGGCACCTGCAACAAACCCTGGACTTGCATCTGCAACGAGGGTTGGGGAAGGC
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TCPQGFYGKNCEIIAMTCADDPCFNGGTCEEKFTGGYVGRCPPFTTGSNCEKRLDRCS
HKPCANGGECVDLGASALCRCRPGFSGSRCETNIDDCARYPCQNAGTCQDGINDYTCT
CTLGFTGKNCSLRADACLTNPCLHGGTCFTHFSGPVCQCVPGFMGSTCEFPQASLEK
MAPRYGQTSPSAVAYSCYLGVLAVFLGVCVGLVYLRRRHRLRRQQLCDSVFNDLETV
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Pred. No. 8.92e-47;
0; Mismatches 135
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XELXDEL 2166 bp 1
Xenopus laevis X-Delta-1
L42229
                                                              Submitted (15-MAY-1995)
Unit, ICRF, Oxford, UK
                                                                                                                                                                                        Chitnis, A., Henrique, D., Lewis, J., Ish-Horowicz, D. and Kintner, C. Primary neurogenesis in Xenopus embryos regulated by a homologue the Drosophila neurogenic gene Delta the Drosophila neurogenic gene Delta Nature 375 (6534), 761-766 (1995)
                                                                                                                                                                                                                                                                                                                        Expression of a Delta homologue in Nature 375 (6534), 787-790 (1995)
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Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; P
Pipidae; Xenopodinae; Xenopus.
1 (bases 1 to 2166)
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Xenopus laevis
                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                      Henrique, D., Adam, J., Myat, A., Chitnis, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delta; Notch; X-Delta-1; neurogenic
                                                                                                                                Ish-Horowicz,D
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                                                                                                                                                  (bases 1 to 2166)
                                                                                                                                                                                                                                                                              (bases 1
                                       Location/Qualifiers
/organism≖"Xenopus laévis'
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/translation="MGQQRMLTLIVLSAVLCQISCSGLFELRLQEFVNKKGLLGNMNC
                                                                                                                                                                                                                      CRPGSLASLORCECKTFFRICLKHYQSNVSPEPPCTYGGAVTPVLGTNSFVVPESSNA
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1 (bases 1 to 3051)
Appel, B. and Eisen, J.S.
Appel, B. and Eisen, J.S.
Esgulation of neuronal specification in the zebrafish spinal cord by Delta function
Development 125 (3), 371-380 (1998)
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1. 3051
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Danio rerio DeltaA (deltaA) mRNA, complete cds.
AF030031
g2809388
                                                 /clone_lib="Chris Kintner's St17"
'note="(vector lambda gt10)
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Appel, B. and Eisen, J.S.
Direct Submission
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Best Local Similarity 67.7%;
Matches 180; Conservative
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/db xref="PID:92809389"
//translation="MNQSAKREAFNTRDPLTDLRSAKLLRDFHKILFIYLFIMGRHLL
//translation="MNQSAKREAFNTRDPLTDLRSAKLLRDFHKILFIYLFIMGRHLL
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SLIIEALHADSKEDLTTENPERIISTWTTQRHLTVGEDWSQDLHSVGRTELKYSYRFV
CDEHYYGEGGGYFCRPRDDAFGHFTGCBRGEITGAGWRGOYTEPLICHGCDBEHGF
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IASDVPWTAVGSGVLLVLLVVACAVVVVCVRSKVQQRRRDREDEVANGENETINNLT
NNCHRDKDLAVSVVGVAPVKNINKKIDFSSDHDDLSLTTEKRSYKTRHAPADYNLVHE
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KPCLMGATCSNTGGGSSTTCSCRDECTSSGASCELERNECTWOPRCNGGSCTDMENTYSC
TCPPGFYGRNCELSAMTCADGPCFNGGRCADNPDGGYFCQCPTGYAGFNCEKTDHCS
SSPCSNGARCVDLVNSYLCQCPDGFTGMNCDRAGDECSMYPCONGGTCQEGASGYMCT
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SKYSESRYSESKYSESKYSESKYSRCIAVFRVSMCVGWCIGIHVGLCRHQIQIRHGDV
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Pred. No. 3.92e-32;
0; Mismatches 164; Indels
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/map-"between 21173 and 2450"
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Sequence 14 from patent US 5670367.
166494
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287. .2695
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Best Local Similarity 62.1%;
Matches 279; Conservative
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                       XLU70843 2869 bp mRNA VRT 01-DEC-1996
Xenopus laevis Notch ligand X-Delta-2 (X-Delta-2) mRNA, complete
                                                                           Submitted (14-SEP-1996) Molecular Neurobiology Lab., The Institute for Biological Studies, 10010 N. Torrey Pines F Jolla, CA 92037, USA
                                                                                                                                                                                                   Jen,W.C., Wettstein,D.A., Chitnis,A.B. and Kintner,C. The Notch ligand, X-Delta-2, mediates segmentation of
                                                                                                                                                                                                                                              Xenopus laevis
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Pipidae; Xenopodinae; Xenopus.
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                       2 (bases 1 to 2869)
Jen,W.C., Wettstein,D.A., Chitnis,A.B.
                                                                                                                                                                      Unpublished
                                                                                                                                                                                    mesoderm in Xenopus embryos
                                                                                                                                                                                                                                                                                                              African clawed frog.
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/organism="Xenopus laevis"
/db_xref="taxon:8355"
398. .2326
                                              1. .2869
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TGCAAATGCGCTCCAGGATACAGTGGTGATGATTGCGAAAATGAGATC 1137
                                                  TGTAGCTGTCGTGCTTCACAGGAACCAATTGTGAAATAGACATC 1324
                                                                                                                                                              AACCACCAGCCATGCCGTAATGGAGCAAGCTGCATCAATATTGGCCAAGGGAGCTACTCT 1276
                                                                                                           AACCACAGACCCTGCAAGAATGGCGGAACCTGCTTCAACACCGGCGAGGGATTGTACACA
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TLGYGGKDCTLRVDACSSKPCKNGGTCYTHFTGNVCQCPTGFMGTSCEFRVHDPTPAS
HRADSSNTLTMVVCLGLLTFFLLGCGVFMVMRGMRRGHFNEKGRVNNDLEPKNNLIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Notch ligand x-Delta-2"
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/translation="MASPLLLVYVAATICLPLVYPAGVFELKIHSFSTPRPACAAGKS
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LIIESWTTNSAEQSTENPDNLLSRLATRRRLSIGEDWSQDIHLGQQSELRYSYHVSCD
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LPGECKCRMGWGGELCDECLRYPGCQHGSCSOPWECICQEGWGGLFCRQDLNYCTNHQ
PCRNGASCLIFIGQGSYSCSCCRAGFTGINCELDINECASNPCKNGGSCNDLENDYECVE
PCRNGASCLIFIGQGSYSCSCCRAGFTGINCELDINECASNPCKNGGSCNDLENDYECVE
PRGFYGKNCDISAMTCEDGPCFNGGTCIEKSSGVGYVCRCPFNYHGSNCEKKIDRCTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHFKMPNPDYLREKSSSKQKLLQGSESEEERSGRRTDRKPDTKQCNPTSRYPEDGAY
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398. .2326
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Pred. No. 4.90e-26;
0; Mismatches 109
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Nmatch

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Dbase 0;

Query 0

Searched: 176886 seqs, 63680241 bases x N

Post-processing: Minimum Match Listing first 45 summaries

Database:

n-geneseq31-2 i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part20 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37

Statistics: Mean 9.863; Variance 5.746; scale 1.716

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| O30997 Delta CDNA D11. Q30997 Delta CDNA D11. Q43911 Sequence encoding a d Q43911 C-Delta-1 gene. T58899 C-Delta-1 gene. T70174 Proliferation and dif T58899 H-Delta-1 gene. T58899 H-Delta-1 contig clon T58899 H-Delta-1 contig clon Q25811 Drosophila SLIT prote T70175 Proliferation and dif T40091 Human Serrate-2 (HJ2) Q43910 Sequence encoding a s T40090 Human Serrate-1 (HJ2) |
|---|
| Description Delta CDNA D11. Sequence encoding a d C-Delta-1 gene (alter C-Delta-1 gene. Proliferation and dif M-Delta-1 contig clon Drosophila SLIT prote Proliferation and dif Human Serrate-2 (HJ2) Sequence encoding a s Human Serrate CDNA. Chick Serrate CDNA. Dase substituted E.co |

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| 4835 5191 | 1438 | 1433 | 1089 | 190 | 178 | 130 | 114 | 114 | 114 | 39 | 565 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 1556 | 204 | 114 | 114 | 114 | 114 | 1573 | 91 | 4 |
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| T3/051 T37050 Q57710 | Q04550 | Q99243 | N92576 | T76452 | T76405 | T76152 | Q70473 | Q70470 | Q70472 | Q51787 | Q35072 | Q70465 | Q70466 | Q70467 | Q70468 | Q70469 | Q70472 | Q70470 | Q70467 | Q68221 | N81164 | Q70465 | Q70468 | Q70469 | Q70466 | Q68222 | Q51746 | Q01/40 |
| Drosophila Fru 2 CDNA Drosophila Fru 1 cDNA Neurocan DNA. | EcoRI-EcoRI fragment | Insulin like growth f | Sequence of the 1.1kd | Chymase antisense oli | Human endothelin-1 an | Human vascular cell a | Generic DNA sequence | DNA | Generic DNA sequence | _ | HCV envelope region n | Generic DNA sequence | DNA | DNA | DNA | Generic DNA sequence | | DNA | Generic DNA sequence | Neuroendocrine tumor | Base substituted E.co | DNA | DNA | | Generic DNA sequence | ine t | | origonucreotide probe |
| 2.08e-04 2.08e-04 2.08e-04 | .08e- | .08e- | .08e- | .08e- | .06e- | .06e- | .06e- | . 08e | .08e | .02€ | .72e | .72e | .72e | . 36e | | .36e | .72e | .72e | . 36e | . 75e | .75e | .02e- | 1.02e-07 | .02e- | .33e- | ٠ | .40e- | .4Ue- |

ALIGNMENTS

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RESULT
AC Q3
AC Q4
AC Q3
AC Q4
Human Notch and Delta DNA and protein sequences - used for study and manipulation of differentiation processes Claim 50; Fig 13; 239pp; English.

The sequence given represents the nucleotide sequence of human Delta gene contained in plasmid cDNA clone Dll. A human expression library was constructed and screening assays were carried out on to select for the expressed Delta product. Alternatively the sequences could be isolated by amplification using polymerase chain reaction (PCR) primers. The isolated gene may be inserted into a cloning vector and expressed. The Delta gene and also the Notch and Serrate neurogenic genes are designated "toporythmic" genes. The proteins they encode are involved in specific homo- or heterotypic interactions crucial to differentiation. The quantitation of mRNA for human Notch and Delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992; U03651.
03-MAY-1991; US-95189.
14-NOY-1991; US-791923.
(INDV ) UNIV INDIANA FOUND.
(UYYA ) UNIV YALE.
Artavanis-Tsakonas S, Blaumueller CM, Fehon RG, Muskavitch MAT;
Rebay I, Shepard SB;
WPI; 92-398861/48.
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Human; Notch; plasmid; cDNA; clone; D11; expression library; PCR; polymerase chain reaction; primer; cloning vector; Delta; Serrate neurogenic; toporythmic; homotypic; heterotypic; differentiation; quantitation; antibody; ss.
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12-NOV-1992.
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Q30997;
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142..2643
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/note= "Delta cDNA D11"
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| adhesive molecules, and study of its expression are possible us DNA and antibodies raised against the Notch and Delta proteins ence 2892 BP; 739 A; 763 C; 808 G; 582 T; | ch il Similarity 99.9%; Score 2888; DB 5; Length 2892; 18 Similarity 99.9%; Pred. No. 0.00e+00; 2890; Conservative 0; Mismatches 2; Indels 0; Ga | gaattcggaggaattattcaaaacataaacacaataaacaattgagtagttgccgcaca | cacacacacacagccgtggttattacactaaagcgacactcaatccaaaatca | gcaacaaaaacatcaataaacatgcattggattaaatgtttattaacagcattcatt | ttoacagtcatcgtgcaggttcacagttccggcagctttgagttgcgcctgaagtacttc | agcaacgatcacgggcgggacaacgaggtcgctgctgcagcggggagtcggacgga | acgggcaagtgcctgggcagctgcaagacgcggtttcgcgtctgcctaaagcactaccag | gccaccatcgacaccacctcccagtgcacctacggggacgtgatcacgcccattctcggc | gagaacteggteaatetgaeegaegeeeagegetteeagaaeaagggetteaegaateee | atccagttcccttctcgttctcatggccgggtaccttctcgctgatcgtcgaggcctgg | catgatacgaacaatagcggcaatgcgcgaaccaacaagctcctcatccagcgactcttg | gtgcagcaggtactggaggtgtcctccgaatggaagacgaacaagtcggaatcgcagtac | acgtcgctggagtacgatttccgtgtcacctgcgatctcaactactacggatccggctgt | gccaagttctgccggcccgcgacgattcatttggacactcgacttgctcggagacgggc | gaaattatetgtttgaccggatggcagggcgattactgtcacatacccaaatgcgccaaa | ggctgtgaacatggacattgcgacaacgcaatcaatgcgtttgccaactgggctggaag | gagccttgtgcaacgagtgcgttctggaaccgaactgcatccatggcacctgcaacaa | GTGCAACGAGTGCGTTCTGGAACCGAACTGCATCCATGGGACTGGCAAC ttgcatctgcaacgagggttggggaggcttgtactgcaaccaggatctg |
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Disclosure; Pages 84-85; 119pp; English.
Delta encodes an approx. 100 kd protein (Delta denotes 'DLZM', the protein product of the predominant zygotic and maternal transcripts) that has nine EGF-like repeats within its extracellular domain. Molecular studies have lead to the suggestion that Notch and Delta constitute biochemically interacting elements of a cell communication mechanism involved in early developmental decisions.
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Disclosure: Fig 1B1-1B2: 135pp; English.
The C-delta-1 gene (T58898) codes for the chick homologue (W00876)
The C-delta-1 gene (T58898) codes for the chick homologue (W00876)
of Drosophila Delta, a protein that binds to Notch protein. It was obtd. by PCR amplification of CDNA from stage 4-6 embryos using primers (see also 759455-56) based on fly Delta sequences. A shorter variant (T58897) was also identified. C-Delta-1 expression appears to be the earliest known marker for prospective neurons. Mouse (T58899) and human (T58900, T59454) Delta-1 sequences have also been isolated. Delta-1 genes can be used in the prodn. of Delta polypeptides and (including antisense sequences) utilised in the treatment of disorders of cell fate or differentiation, such as cancer, and nervous system disorders, or to promote tissue
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           C-Delta-1 gene (alternatively spliced variant).

C'Delta-1; cell proliferation; nervous system disorder;

C'Issue regeneration; Notch; cervix cancer; breast cancer;

lung cancer; colon cancer; melanoma; seminoma;

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Me C-delita.1 gene (TS889) codes for the chick homologue (W11719) of Drosophila Delita, a protein that binds to Notch protein. It was obtd. by PCR amplification of cDNA from stage 4-6 embryos using
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C-Delta-1; cell proliferation; nervous system disorder; tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer; colon cancer; melanoma; seminoma;
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bases 1981-2400 are missing from the
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277..2463
//note= "bases 1201-1260 do not enc
translated sequence for C-Delta-1
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T58897 standard; cDNA; 2088
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28-APR-1997 (first entry)
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28-JUN-1996; U11178.
28-JUN-1995; US-0005
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                                                                                             1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regeneration and repair. Sequence 2088 BP; 4
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                                                             TTGTGCAACGAGTGCGTTCTGGAACCGAACTGCATCCATGGCACCTGCAACAACCCTGG
                                                                                                                           CATG--GACAT-TGCGACAAACCCAATCAATGCGTTTGCCAACTGGGCTGGAAGGGAGCC
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llarity 61.1%;
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Pred. No. 1.05e-
0; Mismatches
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The present sequence encodes a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement blood formation, e.g. after immunosuppression.

Sequence 2663 BP; 534 A; 825 C; 829 G; 475 T;
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T70174;
11-FEB-1998 (fi
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Peptide(s) encoded
proliferation and c
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17-NOV-1995; JP-299611.
(ASAH) ASAHI KASEI KOGYO
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29-MAY-1997.
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                              agcggccgcacggacctcaagtactcctaccgcttcgtgtgtgacgaacactactacgga
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     TCGCAGTACACGTCGCTGGAGTACGATTTCCGTGTCACCTGCGATCTCAACTACTACGGA
                                                                                                       CGACTCTTGGTGCAGCAGGTACTGGAGGTGTCCTCCGAATGGAAGACGAACAAGTCGGAA
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l Similarity 61.88;
514; Conservative
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179..241
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242..2347
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differentiation
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Pred. No. 1.43e-68;
0; Mismatches 305
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946 GGCACCTGCAACAACCCTGGACTTGCATCTGCAACGAGGGTTGGGGAGGCTTGTACTGC 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure: Fig 7A-7B: 135pp; English.

The M-delta-1 gene (T58899) codes for the mouse homologue (W11720) cof brosophila Delta. a protein that binds to whoch protein. It was obtd. by PCR amplification of cDMA derived from 8.5 to 9.5-day mouse embryos using primers (see also T59457-58) based on Delta and ECF-1ike repeat sequences. M-Delta-1 is primarily expressed in the presomitic mesoderm, central nevous system, peripheral nervous system, and kidney. Chick (T58897-98) and human (T5890).

T59454) Delta-1 sequences have also been isolated. Delta-1 genes can be used in the prodn. of Delta polypeptides and (including antisense sequences) utilised in the treatment of disorders of cell facte or differentiation, such as cancer, and nervous system
                                                                                                                                 913
                                                                                                                                                                885
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                                                                                                                                                                                                                             886 CAACTGGGCTGGAAGGGAGCCTTGTGCAACGAGTGCGTTCTGGAACCGAACTGCATCAT 945
                                771
                                                                  gagcgtggggagaaagtgtgcaaccctggctggaaagggccctactgcacagagccgatc 853
                                                                                                 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New vertebrate Delta protein, DNA and antibodies - for treating and preventing cancer, nervous system disorders and for tissue
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                  734 gagggetgetecgtttetgeegteecegggaegatgeetteggeeactteaeetgtggg
                                                                                                 GAGACGGCGAAATTATCTGTTTGACCGGATGGCAGGGCGATTACTGTCACATACCCAAA
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Pred. No. 9.37e-53;
0; Mismatches 294; Indels 16;
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M-Delta-1 gene.
M-Delta-1; cell proliferation; nervous system disorder;
tissue regeneration; Notch; cervix cancer; breast cancer;
lung cancer; colon cancer; melanoma; seminoma;
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28-JUN-1995; US-000589.
(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
(UYYA ) UNIV YALE.
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Best Local Similarity 61.6%;
Matches 498; Conservative
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WPI; 97-100159/09.
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618 GGTGTCCTCCGAATGGAAGACGAACAAGTCGGAATCGCAGTA-CACGTCGCTGGAGTACG
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                                                               accetgcacctacggcagtgccgtcacgccagtgctgggtgtcgactccttcagcctgcc
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29424-1997 (first entry)
H-Delta-1 contig clone HD118.
H-Delta-1; cell proliferation; nervous system disorder; tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer; colon cancer; melanoma; seminoma; neurogenesis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMCR ) IMPERIAL CANCER RES TECHNOLOGY
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28-JUN-1995; US-000589.
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                                   W09210518-A.
25-JUN-1992.
27-NOV-1991; U09055.
07-DEC-1990; US-624135.
(UYYA) UNIV YALE.
Artavanis-Tsakonas S, Ro'
WPI; 92-234590/28.
                                                                                                                                                                                                                                                                                                            Q25811 :
Q25811;
                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                           Drosophila SLIT protein involved in axon pathway development. Neurogenesis; EGF-like repeats; epidermal growth factor; TAGG embryonic CNS; leucine-rich repeat; Flank-LRR-Flank; glial cemotch; axonogenesis; cell-cell interaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single reading frame gave a correct sequence for the H-Delta-1 protein. Predicted amino acid sequences for all 3 reading frames (W11725-27) were detd. and sequences (W11728-38) showing homology to chick and mouse Delta-1 (W11719-20) sequences were identified. The H-delta-1 gene can be used in the prodn. of H-Delta-1 polypeptides and (including antisense sequences) used to treat disorders of cell fate or differentiation, such as cancer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p-PSDB; W11726;
p-PSDB; W11727.
New vertebrate Delta protein, DNA and antibodies -
preventing cancer, nervous system disorders and for
 SLIT protein and sequence elements f neuro-degenerative disease - useful
                                                                                                                                                                                                          5'utr
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A contig sequence (T59454) of H-Delta-1 gene was obtd. from clone HD118, which was isolated from foetal brain library using a partial sequence as probe. Errors in the sequence meant that no
                          P-PSDB;
                                                                                                                                           3'utr
                                                                                                                                                                                                                                 Drosophila melanogaster.
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Similarity 71.9%;
166; Conservative
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4755..8378
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315..4757
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d. No. 2.71e-45;
Mismatches 64
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No. 2.
              for treating
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RESULTATION AND THE PRINCIPAL 
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PCR and standard library screening techniques were used to further analyse previously isolated slit cDNA clones. A cDNA clone representing the 5' most 2.4kb of sequence was isolated from a larval library and PCR was used to isolate a corresp. sequence from a 4-8 hour embryonic library. Two forms of the SLIT message were identified differing by 33 nucleotides. Genomic and cDNA sequencing indicates the transcripts consists of an approximately 314bp 5' untranslated leader sequence, followed by either-a 4407bp or 4440bp ORF depending on the splice form and a 4kb 3'.UTR.

Sequence 8378 BP; 2192 A; 2272 C; 2164 G; 1742 T;
                                                                   Claim 15; Page 82-91; 114pp; Japanese.

The present sequence encodes a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement blood formation, e.g. after immunosuppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-1997.
15-NOV-1996;
30-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proliferation and differentiation suppression protein encoding Proliferation; differentiation; suppression; human; delta-1; serrate-1; blood cell; neuron; leukaemia; malignant tumour;
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                                                    Sequence
                                                                                                                                                                                                                                                                          Peptide(s) encoded proliferation and o
                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-1996; J03356.
30-NOV-1995; JP-311811.
17-NOV-1995; JP-299611.
(ASAH) ASAHI KASEI KOGYO
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97-298110/27.
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Similarity 63.9%;
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2.97e-17;
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                                                                                                                                            tgcatggaaggctggatgggccccgaatgtaacagagctatttgccgacaaggctgcagt 1125
                                                                                                                                                                                              cctaagcatggctcttgcaaactcccaggtgactgcaggtgccagtacggctggcaaggc 1185
                                                                                                                                                                                                                                               ctgtactgtgataagtgcatcccacacccgggatgcgtccacggcatctgtaatgagccc 1245
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                                                                                                                                                                                                                                                                                                                             964 TGGACTTGCATCTGCAACGAGGGTTGGGGAGGCTTGTACTGCAACCAGGATCTGAACTAC 1023
                                                                                                                 730 TGCCGGCCCCGCGACGATTCATTTGGACACTCGACTTGCTCGGAGACGGGCGAAATTATC 789
                                                                                                                                                                                                            670 GAGTACGATTTCCGTGTCACCTGCGATCTCAACTACGGATCCGGCTGTGCCAAGTTC 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prevent malignancies characterised by increased Notch activity. Disclosure; Page 98-103; 161pp; English.

Disclosure; Page 98-103; 161pp; English.

CDNA clones (140090 and 140091) respectively code for human Serrate-1 (W05833) and human Serrate-2 (W05833), ligands for Notch that are believed to play a major role in determining cell fates in the central nervous system. The clones were isolated from a foetal brain cDNA library using probes obtd. by PCR amplification of human placental cDNA with primers based on conserved sequences of brosophila Serrate and Delta. The CDNA can be incorporated into vectors and utilised in the treatment and diagnosis of disorders of
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Serrate-2 (HJ2) cDNA (containing an internal deletion).
Serrate-2; human jagged-2; HJ2; Notch; cell differentiation;
cell fate; central nervous system; cancer; tissue repair; therapy;
diagnosis; ds.
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/note= "there is a deletion of approx. 120
nucleotides in this region of the sequence,
probably resulting from a cloning artifact
in construction of the library, encoding a
ored. No. 1.23e-16;
0; Mismatches 158; Indels
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(UYA.) UNIV YALE.
Artavanis-Tsakonas S, Gray GE, Henriq
Lewis JH, Mann RS, Myat AM;
WPI; 96-425379/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
 Pred.
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T40091 standard; cDNA; 4483 BP.
 60.1%;
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          247; Conservative
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240..241
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07-MAR-1996; U03172.
07-MAR-1995; US-400159.
 Similarity
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 Best Local
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Principle Accordate protein, nucleic acid and antibodies - used in the study and manipulation of differentiation and other the study and manipulation of differentiation and other physiological processes a physiological processes a Claim 39; Pages 74-80; 119pp; English.

Two Drosophila ganomic phage libraries were screened and recombinant connes were isolated. The CDNAs in lambda 910 were isolated from an early pupal library. The Cl CDNA was isolated from an early pupal library. The Cl CDNA was isolated using the 5' 700 bp; cerminal fragment of the Cl CDNA as probe. The complete 556lbp sequence of DNAs (Q4340). The deduced protein was derived from Cl and C3 cDNAs (Q4340). The deduced protein product appears to be peptide; and S42-564 represent potential membrane associated region; as 1221-145 represent the putative transmembrane domain.

Sequence 5561 BP; 1398 A; 1447 C; 1504 G; 1212 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              740 gacctgaactactgtggcagccaccaccctgcaccaacggaggcacgtgcatcaacgcc 799
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                                                                                                                                                                                                                                                               620 ggctggcaagggaggttctgcgatgagtgtgtcccctaccccggctgcgtgcatggcagt 679
                                                                                                                                                                                                                                                                                                        935 ACTGCATCCATGCCACCTGCAACAA-A-C-CCTGGACTTGCATCTGCAACGAGGGTTGGG
cell fate and differentiation, antisense sequences can be used treat malignancies of cell types that express Serrate or Notch. Sequence 4483 \ BP; 780 \ A; 1389 \ C; 1472 \ G; 842 \ T;
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                                                                                                                          Score 51; DB 24; Length 4483;
Pred. No. 2.09e-15;
0; Mismatches 65; Indels
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Sequence encoding a serrate protein.
Serrate; toporythmic protein; family; ss.
Drosophila melanogaster.
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442..4653
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Matches 134; Conservative
                                                                                                                                                               Local Similarity 64.1%;
nes 116; Conservative
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Matches 24
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2 cDNA clones (T40090 and T40091) respectively code for human Serrate-1 (W05833) and human Serrate-2 (W05833), ligands for Notch that are believed to play a major role in determining cell fates in the central nervous system. The clones were isolated from a foetal brain cDNA library using probes obtd. by PCR amplification of human placenta cDNA with primers based on conserved sequences of Drosophila Serrate and Delta. The cDNA can be incorporated into vectors and utilised in the treatment and diagnossis of disorders of cell fate and differentiation; antisense Serrate sequences can be used to treat malignancies of cell types that express Serrate or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T40090
T40090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Serrate-1 (HJ1) cDNA.
Serrate-1; human jagged-1; HJ1; Not cell fate; central nervous system; diagnosis; ds.
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                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W05833.
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                                                                                                         790
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                          ctgtactgtgataagtgcatcccacacccgggatgcgtccacggcatctgtaatgagccc
                                                      G--AA-CATGGACATTGCGACAAACCCCAATCAATGCGTTTGCCCAACTGGGCTGGAAGGGA
                                                                            cctaagcatgggtcttgcaaactcccaggtgactgcaggtgccagtacggctggcaaggc
                                                                                                        TGTTTGACCGGATGGCAGGGCGATTACTGTCACATACCCAAATGC-GCCAAAG--GCTGT
                                                                                                                                                                        tgccgccccagagatgacttctttggacactatgcctgtgaccagaatggcaacaaaact
                                                                                                                      tgcatggaaggctggatgggccccgaatgtaacagagctatttgccgacaaggctgcagt
                                                                                                                                                            TGCCGGCCCCGCGACGATTCATTTGGACACTCGACTTGCTCGGAGACGGGCGAAATTATC
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Similarity 60.1%;
247; Conservative
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/*tag= c
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410..457
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RESULT
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08-NOV-1990

N81164;

Base substituted E.coli be E.coli beta galactosidase Escherichia coli.

(first entry

beta-galactosidase se alpha-fragment; l

alpha-fragment.

LT 14 N81164

standard;

DNA;

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Query Match
Best Local
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07-MAR-1996; U03172.
07-MAR-1995; US-400159.
(IMCR ) IMPERIAL CANCER R
(UYYA ) UNIV YALE.
Artavanis-Tsakonas S, Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T40092
                                                                                                                                                                                                                              Vertebrate Serrate protein and related DNA - used to treat or prevent malignancies characterised by increased Notch activity. Disclosure; Page 107-112; 161pp; English.

A cDNA clone (T40092) codes for chick Serrate (W05835), a ligand for Notch that is believed to play a major role in determining ce fates in the central nervous system. It was obtd. from an optic explant cDNA library using primers (see also T40094 and T40097) designed to recognise peptide motifs found in both Drosophila Del and Serrate proteins, and rescreening of the library using amplif clones. C-Serrate is expressed in the central nervous system, cranial placodes, nephric mesoderm, vascular system, and limb bud mesenchume
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-Serrate; Notch; cell differentiation; cell fate; tissue repair; central nervous system; cancer; therapy; diagnosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal_peptide
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            caccctgtttgaatggtggtacctgcagcaacactggc
                                                                 gtgaaaccaactggggtggtcagctctgtgaccaaagaccttgaactactgtggaacccacc 832
                                                  tgtgggactcatcagccgtgtctcaacggggggaacttgtagcaacacaggc
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l Similarity 65.8%;
104; Conservative
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end of the signal peptide is n
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Mismatches 54;
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US-08-083-590A-1.rng

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Lehtowara P. Knowles J. Koivula A. Bamford J. Reinikainen T. WPI: 88-27927/40.

Throducing random point mutations into nucleic acods - Introducing random point mutations into nucleic acods - Introducing random point mutation of molecules and screening.

The preparation, completion of molecules and screening.

The sclosure: p. English.

Random point mutations were introduced into the alpha fragment of E. Coli beta galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminete at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are emplated to forms that can be amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which see also P86575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 vgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybb 140
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Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
(Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
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Q51746 standard; CDNA; 91 BP.
Q51746;
31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 204;
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Pred. No. 8.69e-12;
55; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 9; Length 91;
Pred. No. 3.40e-11;
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          /*tag= a
/function=multiple cloning site
187..204
/*tag= b
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Location/Qualifiers
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01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-378844/48
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Matches 13; Conservative
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                                                                                                                                               US-034819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 BP;
Key
misc_feature
                                                                                                                                 30-MAR-1988;
                                                                                                                                                03-APR-1987;
                                                                                                EP-285123-A
                                                               primer_bind
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4; Indels

44; Mismatches

4; Conservative

Best Local Similarity

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2167 GCCGCGAACCCGAATATCATCAAAAACACCTGGGACAAGTCGGTCAACAACA 2218
7 ggcgssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhvyv 58
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Search completed: Sat Jun 13 10:07:04 1998 Job time : 617 secs.

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| Release | <u></u> |
| 3.1A | |
| John F. | |
| Collins, | |
| Release 3.1A John F. Collins, Biocomputing Research Unit. | |
| ng Research | [====] |
| Unit. | , , |
| 1 | (MT) |

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Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Sat Jun 13 10:07:22 1998; MasPar time 126.49 Seconds 1205.088 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: N.A. Sequence: Title: >US-08-083-590A-1 (1-2892) from US08083590A.seq 2892

Comp:

Scoring table: TABLE default Gap 6

Nmatch STD •• Dbase 0; Query 0

102132 seqs, 26354270 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 9.454; Variance 5.035; scale 1.878

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| ì | 74 | 5275 | 5191 | 5191 | 1425 | 1425 | 1320 | 4835 | 4255 | 7218 | 1556 | 1556 | 215 | 1573 | 1573 | 215 | 8378 | 7218 | 2892 | Length |
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| PODITION | ~ | Applicatio | Applicati | Applicati | Applicatio | Applicati | Applicatio | |
| 7.300-02 | 7.36e-02 | 1.20e-04 | 1.20e-04 | 1.20e-04 | 1.67e-03 | 1.67e-03 | 1.67e-03 | 8.10e-06 | 8.10e-06 | 1.74e-09 | 7.35e-09 | 7.35e-09 | 9.50e-11 | 4.96e-12 | 4.96e-12 | 4.96e-12 | 5.18e-20 | 6.66e-32 | 0.00e+00 | Pred. No. |

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| 2 K 6 6 | 25 | 27 | 27 | 26 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 26 | 25 | 25 | 25 | 25 | 27 | 26 | 25 | 26 | 25 | |
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| 35100 | 11613 | 5775 | 5775 | 5288 | 4978 | 2968 | 2950 | 2003 | 2003 | 2003 | 2003 | 1383 | 1201 | 745 | 745 | 745 | 242 | 242 | 105 | 82 | 81 | 81 | |
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| DS-08-306- | US-08-484- | PCT-US93-0 | US-08-306- | PCT-US95-1 | US-08-220- | PCT-US93-0 | PCT-US93-0 | US-08-469- | US-08-249- | US-08-036- | PCT-US94-0 | US-08-484- | 5252556-2 | US-08-249- | US-08-036- | PCT-US95-0 | US-08-273- | US-08-273- | US-07-865- | PCT-US95-1 | PCT-US95-1 | PCT-US95-1 | |
| Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Patent No. 5252556 | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | |
| 19, | 10, | 29, | 15, | 18, | 1 | , | 7, | 21, | 21, | 21, | 21, | | 5 | 163 | 163, | 163 | 1 | 1, | 13, | 97, | 92, | ,86 | |
| Applicati | Applicati | Applicati | Applicati | Applicati | Applicatio | Applicatio | Applicatio | Applicati | Applicati | Applicati | Applicati | Applicatio | 252556. | 163, Applicat | , Applicat | 163, Applicat | Applicatio | Applicatio | Applicati | Applicati | Applicati | Applicati | |
| 2.13e-02 2.13e-02 | • | 6.02e-03 | 6.02e-03 | | | | 7. | 7.36e-02 | 7.36e-02 | 7.36e-02 | 7.36e-02 | 7.36e-02 | 2.13e-02 | | 7.36e-02 | 7.36e-02 | 7.36e-02 | 6.02e-03 | 2.13e-02 | 7.36e-02 | 2.13e-02 | 7.36e-02 | |

ALIGNMENTS

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEPAN: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5: US-08-264-534-5 STANDARD; DNA; UNC; 2892 BP. Sequence 5, Application US/08264534 Sequence 5, Application US/08264534 Patent No. 5648464 01-JAN-1900 XXXXXX GENERAL INFORMATION: APPLICANT: Artava ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk SEQUENCE CHARACTERISTICS: LENGTH: 2892 base pairs TYPE: nucleic acid COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,534
FILING DATE: CORRESPONDENCE ADDRESS: TITLE OF INVENTION: NUMBER OF SEQUENCES: STREET: CITY: N STATE: COUNTRY: STRANDEDNESS: ADDRESSEE: New York New York
Y: U.S.A. 1155 Avenue of the Americas Artavanis-Tsakonas, Spyridon et al.

VENTION: Human No. 5648464ch And Delta, Binding Domains

VENTION: In Toporythmic Proteins, And Methods Based Thereon Pennie & Edmonds 07/695,189 7326-004

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Pred. No. 0.00e+00;
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TOPOLOGY: unknown MOLECULE TYPE: CDNA FEATURE:
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                                     GENERAL INFORMATION:
 APPLICANT:
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APPLICANT:
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                                                                                                         STANDARD;
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CLONE: pTZgpt-F1s
Sequence 7218 BP; 1944 A; 1491 C; 1486
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP 9:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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STREET: 1800 Diag
CITY: Alexandria
STATE: VA
COUNTRY: USA
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                     CACTCCCGCCGCCGAACGAGGGCCAACGCTGGCTACAGTAGGAACCCTCGCCTAAAAC
                                          CCCCGCTCCGCTGCCGCTGCCGAAGCTGCAGCCATTAGCTGGGATGAACAGGCTCCGGC
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TOPOLOGY: lir
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Sequence 1, Application PC/TUS9109055
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Sequence 1, Application PC/TUS9109055
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon
TITLE OF INVENTION: Purified SLIT protein and Sequence Elements Thereof
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yale University
ADDRESSEE: Vale University
STREET: 246 Church Street
STREET: Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila Melanogaster
DEVELOPMENTAL STAGE: embryonic and larval, germ-line
IMMEDIATE SOURCE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 800 Kb storage
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CLONE: be2.4, ka2.4, B52-2, B52-5, smart2-19
POSITION IN GENOME:
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 T 3
PCT-US91-09055-1 STANDARD; DNA; UNC; 8378 BP
                                                                                                                                                                                                                COMPUTER: Apple Macintosh COMPUTER: Apple Macintosh 6.0.5 SOFTWARE: Microsoft word 4.0 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION UNBER: PCT/US91/09055 FILING DATE: 19911127 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION UNBER: US/07/624,135 FILING DATE: 7-DEC-1990 ATTORNEY/AGENT INFORMATION: NAME: Barth, Richard ATORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: 28,180 REFERENCE/DOCKET NUMBER: 900964/RSB TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION FOR SEQ ID NO: 1: SUGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1 to 314
IDENTIFICATION METHOD: experimental
NAME/KEY: Translated region
LOCATION: 315 to 4754
IDENTIFICATION METHOD: experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: 5' leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: 3' untransiaticCATION: 4755 to 8378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHROMOSOME/SEGMENT: 2R
MAP POSITION: 52D
UNITS: chromosome band
                                                                                                                                             CITY: New Haven
STATE: Connecuticut
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 8378
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: no
ORIGINAL SOURCE:
                             01-JAN-1900
                     XXXXXX
RESULT
ID PC
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                                                                                                                                                                                                                                 1645 AATGGAGGAACCTGCTTGAATCTCAACAACGATTACCAGTGCACCTGTCGGGGATTT 1704
                                                     3417 TGGGGGAATGGAGCCAAGTGCATGGACCACTTACCCACTACAGCTGCGATTGTCAGGCA 3476
                                                                                                                                   3477 GGTTTCCATGGCACCAACTGCACGGACAATATTGACGACTGCCAGAACCACATGTGCCAG 3536
                                                                                                                                                         1585 GGTTTCCATGGCACCCACTGTAGTAGCAAAGTTGACTTGTGCCTCATCAGACCGTGTGCC 1644
                                                                                                                                                                                                               3537 AACGGTGGAACGTGCGTGGACGGCATCAACGACTACCAATGCCGCTGTCCAGACGACTAT 3596
                                                                                           Gaps
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OTHER INFORMATION: /standard_name- "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
Sequence 215 BP; 15 A; 8 C; 25 G; 26 T; 141 other;
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
Best Local Similarity 63.9%; Pred. No. 5.18e-20;
Matches 124; Conservative 0; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2307E-540
                                                                                                                                                                                                                                                                                                                                                                                                        US-08-238-163-5 STANDARD; DNA; UNC; 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/POCKET NUMBER: 2307
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEO ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 215 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                        3597 ACGGCCAAGTACTG 3610
                                                                                                                                                                                                                                                                                                              1705 ACTGGCAAGGATTG 1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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DB 1; Length 215;

1.5%; Score 42;

Query Match

Length 8378;

DB 2;

1.9%; Score 54;

Query Match

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910

1090

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Query Match
Best Local S
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                            Matches
                                                                          ORIGINAL SOURCE:
STRAIN: Mouse
Sequence 1573 BP; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application Sequence 4, Application Patent No. 5580738 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-597-545-4
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  234 ATGGATTCTGCGAGGCTGACAATGTCTGCAGGTGCCATGTTGGCCTGGGAGGGTCCCCTCT 293
                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 CAGATTGACCGAGTTCTCGCCGAGAATGGGCGTGATCACGTCCCCGTAGGTGCACTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 YN--YGGNNVGAAKTHYYTHTNVSGADSKTVTDS-YNASGTSSSNGGTDGNRSGADSYGS 122 : | :| :| :| :| :| :| :| :| :|
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMMANDE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 MSSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSAN
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,537
FILING DATE: 11-DEC-1992
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/597,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LABORDA, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                        FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAGAAGGGGAACTGGATGGGATTCGTGAAGCCCTTGTTCTGGAAGCGCTGGGCGTCGGT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTKSNVSNNCGGGNKRDVSSYANNKCCG
                                                                                                                STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                      TELEFAX:
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                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                      LENGTH:
                                       Similarity
                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington, D.C.
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                           Conservative
                                                                            Mouse Dlk
BP; 327 A; 507 C; 419 G;
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                                                                                                                  linear
                                      1.5%;
                                                                                                                               double
                                                                                                                                                                                                                                                                                                                                        435
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Delta-Like Gene Expressed
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US/08597545
                                                                                                                                                                                                                                                         29,768
                                      Score 42; DB 1; I
Pred. No. 4.96e-12;
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                           0
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                          Mismatches 140;
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                                                                            320 T;
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                           Indels
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Query Match
Best Local Similarity
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Sequence 4, Application US/08457135
Patent No. 5644031
                                        Sequence
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US-08-457-135-4
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                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: 01-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/989
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.76
                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414
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                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                               ORIGINAL SOURCE:
                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1573 base pairs
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LABORDA, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAATGGTTCTCCCTGCCAGCACGAGGCGCCCTGCGTGGATGA 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATCTGCAAGGATGGCTGGGACGGGAAATTCTGCGAAATAGACGTTCGGGCTTGCACCT 413
                                                                                                                                                                                                                                                                                                                                                                                                               STREET: July STREET, Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGATGTCAATCCCTGCCAGAATGGTGGTACCTGCATCGATGA 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- CA-ACCCCCTGCGCCAACAATGGAACTTGCGTGGACCTGGAGAAAGGCCAGTACGAAT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAACGAGTGCGTTCTGGAACCGAACTGCATCCATGGCACCTGCAACAAACCCTGGACTT 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGACAAGTGTGTAACTGCCCCTGGCTGTGTCAATGGAGTCTGCAAGGAACCATGGCAGT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGACATTGCGACAAACCCCAATCAATGCGTTTGCCAACTGGGCCTGGAAGGGAGCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAAATGCGCTCCAGGATACAGTGGTGATGATTGCGAAAATGAGATCTACTCCTGCGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCATCTGCAACGAGGGTTGGGGAGGCTTGTACTGCAACCAGGATCTGAACTACTGCACCA 1030
                                                                              TOPOLOGY:
                                                                                      STRANDEDNESS:
                                                                                                                                                        TELEX:
                                                                                                                                                                  TELEFAX:
                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                       1573 BP; 327 A;
                                                                                                                                                                                                                                                                                                                                                                                                    20007-5109
                                                                                                     nucleic acid
                                                                                                                                                         904136
                                                                                                                                                                                                                                                                                                                                                                                                                                     3000 K Street,
                                                                                                                                                                  :: (202)672-5300
(202)672-5399
                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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  1.5%;
                                                                                          double
                                        A; 507
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Delta-Like Gene Expressed
                                                                                                                                                                                                                                                                                                                                     Release #1.0,
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                                                                                                                                                                                                                   29,768
  Score 42; DB 1; I
Pred. No. 4.96e-12;
                                       C; 419 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                         N.W.,
                                                                                                                                           4.
                                                                                                                                                                                                        40399/304/NIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                         Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumors
              DB 1;
                                        320 T;
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              Length 1573;
                                        0 other;
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66 YNYG-GNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGT-DGNRSGADSYGSS 123
                                                                                                                                                                                      6 MSSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSAN 65
                                                                                                                                                   Gaps
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;
                                                                                                                                                   ;
               LOCATION: 1..215
OTHER INFORMATION: Sequence of PGIP from bean."
Sequence 215 BP; 15 A; 8 C; 25 G; 26 T; 141 other;
                                                                                                                                                                                                                                                                                                                                                            2003 GCAAGCGTAGCTCAGGAAAAGGACGAGGAGGCCAGGAAGC 2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 1; Length 1556;
Pred. No. 7.35e-09;
0; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                          124 KTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGS 171
                                                                                                          Query Match 1.4%; Score 40; DB 1; Length 215; Best Local Similarity 16.7%; Pred. No. 9.50e-11; Matches 28; Conservative 71; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,135
FILING DATE: 01-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/989,537
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BEAT: Scephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/304/NIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: Human Dlk
Sequence 1556 BP; 302 A; 514 C; 440 G; 300 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Delta-Like Gene Expressed In
TITLE OF INVENTION: Delta-Like Gene Expressed In
TITLE OF INVENTION: Neuroendocrine Tumors
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STRENSESE: Folew:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-457-135-3 STANDARD; DNA; UNC; 1556 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08457135. Sequence 3, Application US/08457135 Patent No. 5644031 GENERAL INFORMATION: APPLICANT: LABORDA, Jorge
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TELEPHONE: (202)672-5300
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 1556 base pairs
NAME/KEY: misc_feature
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Best Local Similarity 57.5%;
Matches 199; Conservative
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STRANDEDNESS: double
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Sequence 5, Application US/08238163
APPLICANT: BENNETT, Alan
APPLICANT: BENNETT, Alan
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend Rhourie and Crew
                                                                                                                                                                                                            1091 GCAAATGCGCTCCAGGATACAGTGGTGATGATTGCGAAAATGAGATCTACTCCTGCGATG 1150
                                                                                                                                                                                                                                                                 414 --CA-ACCCCCTGCGCCAACAATGGAACTTGCGTGGACCTGGAGAAAGGCCAGTACGAAT 470
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                                                          354 GCATCIGCAAGGAIGGCIGGGACGGGAAATICIGCGAAAIAGACGIICGGGCTIGCACCI 413
                                     234 ATGGATICTGCGAGGCTGACAATGTCTGCAGGTGCCATGTTGGCTGGGAGGGTCCCCTCT 293
                                                                                                                294 GIGACAAGIGIGIAACIGCCCCIGGCIGIGICAAIGGAGICIGCAAGGAACCAIGGCAGI 353
3; Gaps
0; Mismatches 140; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     531 TCAATGGTTCTCCCTGCCAGCACGCGCGCCTGCGTGA 573
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REGISTATION NUMBER: 34,774
REFERENCE,DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 543-9600
TELEFAX: (415) 543-9600
INFORMATION FOR SEQ ID NO: 5:
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ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
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STATE: California
 Conservative
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01-JAN-1900
 Matches
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APPLICANT: LABORDA,
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 STRAIN: Human Dlk
Sequence 1556 BP; 302 A; 514 C;
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                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,537
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                             TELEX: 904136
INFORMATION FOR SEQ ID NO:
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          TOPOLOGY: line
ORIGINAL SOURCE:
STRAIN: Human
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1556 base pairs
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                                              TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C.
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Application
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US/08597545
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Best Local S
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GENERAL INFORMATION:
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                                          APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 20,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
INFORMATION
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                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
   TELEFAX: (, c)
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                            TELEPHONE:
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                                                                                                                            FILING DATE:
                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
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CITY: Alexandria
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                                                                                                                                      APPLICATION NUMBER:
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FOR SEQ ID NO:
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                    (703)683-4109
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                                (703)836-9300
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Pred. No. 7.35e-09;
0; Mismatches 144
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STRANDEDNESS:
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                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                      Sequence 14, Application PC/TUS9602331.
Sequence 14, Application PC/TUS9602331
GENERAL INFORMATION:
APPLICANT: The Application of Trustees of the Leland Stanford Junior APPLICANT: Board of Trustees of the Leland Stanford Junior APPLICANT: Board of Reagents, The University of Texas System TITLE OF INVENTION: Methods and Compositions for Altering TITLE OF INVENTION: Sexual Behavior NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT2GPL-F1s
Sequence 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 other;
                                                                                   y Match 1.3%; Score 38; DB 1; Length 7218; Local Similarity 2.0%; Pred. No. 1.74e-09; hes 4; Conservative 116; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: PCT/WS96/02331
FILING DATE: 09-FBB-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                     T 11
PCT-US96-02331-14 STANDARD; DNA; UNC; 4255 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                 E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38 615
REFERENCE/DOCKET NUMBER: 8600-0153.41
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,495
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       1242 YYYYYYYYYYYYYYYYYYYY 1263
                                                                                                                                                                                                                                                   510 GGGTACCTTCTCGCTGATCGTC 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4255 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 350 Camb
CITY: Palo Alto
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Sequence 9, Application PC/TUS9602331
Sequence 9, Application PC/TUS9602331
GENERAL INFORMATION:
APPLICANT: University
APPLICANT: Board of Trustees of the Leland Stanford Junior APPLICANT: Board of Reagents, The University of Texas System TITLE OF INVENTION: Methods and Compositions for Altering TITLE OF INVENTION: Sexual Behavior
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                       Length 4255;
                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: fruitless transcript in Fig. 7E
                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 1507..4032
Sequence 4255 BP; 1273 A; 1130 C; 1000 G; 852 T; 0 other;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: PCT/US96/02331
FILING DATE: 09-PEB-1996
                                                                                                                                                                                                                                                                                                                                                              2073 CTCGGCGGCAGCAGCGGCGGCGGCAGCAGCAGCGG 2110
                                                                                                                                                                                                                                                                                                                                                                                       2226 CTCAGCAGCAGCAGCGGCGGCGGCGGCAGCAGCGGCG 2263
                                                                                                                                                                                                                                                                     Score 32; DB 2; Le
Pred. No. 8.10e-06;
0; Mismatches 3;
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: 350 Cambridge Avenue, Suite 250
Palo Alto
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PCT-US96-02331-9 STANDARD; DNA; UNC; 4835
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,495
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Fru#1 CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERICTICS:
LENGTH: 4835 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                            MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                       Query Match 1.1%;
Best Local Similarity 92.1%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: double
double
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Best Local S
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Best Local Similarity 92.1%;
Matches 35; Conservative
                                                                                       Matches
1192 CGTCCGCGGGACGATCAGTTCGGTCACGCCTGCGGCTCCGAGGGTCAGAAGCTCTGC 1251
                                                             1132 TACCGTGTCCGGGTGCAATGCGCCGTTACCTACTACAACACGACCTTGCACGACCTTCTGC 1191
                                                                                                                                   Sequence 1320 BP; 377 A; 342 C; 333 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08264534 Sequence 8, Application US/08264534
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Sequence 4835 BP; 1462 A; 1223 C; 1106 G; 1044 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-264-534-8 STANDARD; DNA; UNC; 1320
                                      673
                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
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                                                                                    y Match 1.0%;
Local Similarity 59.6%;
hes 87; Conservative
                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,189
FILING DATE: 03-MAX-1991
ATTORNEY/AGENT INFORMATION
NAME: MISTOCK, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,534
                                                                                                                                                                           FEATURE:
                                                                                                                                                                                       MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                      TACGATTTCCGTGTCACCTGCGATCTCAACTACTACGGATCCGGCTGTGCCAAGTTCTGC
                                                                                                                                                   NAME/KEY: CDS
LOCATION: 442
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                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                      1320 base pairs
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                                                                                                                                                                                                                                                                                      212 8698864/9741
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VENTION: Human No. 5648464ch And Delta, Binding Domains
VENTION: In Toporythmic Proteins, And Methods Based The
                                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                      18,872
                                                                                   Score 28; DB 1; I
Pred. No. 1.67e-03;
0; Mismatches 59
                                                                                                                                                                                                                                                                 <u></u>
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Pred. No. 8.10e-06;
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                                                                                                                                       268 T; 0 other;
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Sequence 1, Application US/08385500

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DNA; UNC;

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                                              Matches
                                                          Best
                                                                  Query Match
 2228 CAGCAGCAGCGGCGGCGGCGGCAGCAGCGGC 2261
                                                                                         LOCATION: 92..1213
OTHER INFORMATION:
OTHER INFORMATION:
Sequence 1425 BP; 437 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application Sequence 1, Application Patent No. 5710026
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                                                                                                                                                                                                                                  TELEFAX: (415) 543-50 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            733 CGGCCCCGCGACGATTCATTTGGACACTCGACTTGCTCGGAGACGGGCGAAATTATCTGT 792
                                       1.0%;
Local Similarity 91.2%;
nes 31; Conservation
             37 CAGCAGCGGCGGCGGCGGCGGCAGCAGCAGC 70
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1425 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/385,500
APPLICATION NUMBER: 08-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                    FEATURE:
                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                        TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGACCGGATGGCAGGGCGATTACTG
                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 05-JUN
                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                    single
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US/08464148
                                                                                         /product= "CYTOPLASMIC
ANTIPROTEINASE-2 PROTEIN"
301 C; 357 G; 330 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                          Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                  US/08/464,148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; UNC;
                                                        Score 28; DB 1; 1
Pred. No. 1.67e-03;
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                                              Mismatches
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                                                                  Length 1425;
                                              Indels
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APPLICANT: Sprecher, Cindy A.

TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STRATE: California
COUNTRY: 0S
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/385,500
FILING DATE: US/08/385,500
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Pred. No. 1.67e-03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 92..1213
OTHER INFORMATION: AVIIPROTEINNSE-2 PROTEIN"
Sequence 1425 BP; 437 A; 301 C; 357 G; 330 T; 0 other;
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: PAINELE, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 11,990
REFERENCE/DOCKET NUMBER: 13952-21
TELEPHONE: (206) 467-9600
TELEPHONE: (206) 467-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1425 base pairs
TYPE: nucleic acid
STRANDENESS: single
Sequence 1, Application US/08385500 Patent No. 5712117 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.2%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
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Search completed: Sat Jun 13 10:10:43 1998 Job time : 201 secs.

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MPsrch_nn n.a. - . n.a. database search, using Smith-Waterman algorithm

Run on: Sat Jun 13 08:37:40 1998; MasPar time 2790.42 Seconds 1384.359 Million cell updates/sec

Tabular output not generated.

Title: >US-08-083-590A-1 (1-2892) from US08083590A.seq 2892

Description: Perfect Score: N.A. Sequence: 1 GAATTCGGAGGAATTATTCA......GCCGTTTCGATCCCGAATTC
CTTAAGCCTCCTTAATAAGT......CGGCAAAGCTAGGGCTTAAG 2892

Scoring table: TABLE default Gap 6

Nmatch STD Dbase 0; Query 0

Searched: 1759237 seqs, 667866413 bases × 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: embl-est54

Database: genbank-est106 :em_est1 2:em_est3

3:gb_est1 4:gb_est10 5:gb_est11 6:gb_est12 7:gb_est13
8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est12
12:gb_est18 13:gb_est19 14:gb_est2 15:gb_est20
16:gb_est21 17:gb_est22 18:gb_est3 19:gb_est4 20:gb_est5
21:gb_est6 22:gb_est7 23:gb_est8 24:gb_est9 25:gb_gss
26:gb_sts

Statistics: Mean 11.911; Variance 2.337; scale 5.097

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|) | a | 0000 | × |
|---|--|--|-------------------------------|
| 12 13 | 10 9 10 | 654321 | Result No. |
| 42 42 | 51 51 51 | 436 377 150 78 60 57 | Score |
| 1.5 1.5 | 1.8 1.8 | 15.1 13.0 5.2 2.7 2.1 2.0 | Query Match |
| | | 442 379 568 567 252 247 | % Query Match Length DB |
| 14 10 23 | 13 23 23 | 13 13 13 13 | DB |
| R18606 AA619107 AA024229 | AA754459 AA051023 AA754458 AA046860 | AA538738 AA540186 AA142228 AA015264 AA754459 AA754458 | ID |
| yf96f10.rl Homo sapien vo68b02.rl Soares mous | TRIR | LD18334.5prime LD Dros LD19584.5prime LD Dros CK00091.3prime CK Dros mh30d12.r1 Soares mous 97SN1787 Rice Immature | Description |
| 1.82e-42 2.96e-29 2.96e-29 | | 0.00e+00 0.00e+00 2.05e-235 5.84e-93 6.76e-60 1.40e-54 | Pred. No. |

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| 44 | 42 | 41 | 40 | ω Θ | 37 | 36 | ω 5 | ₩ (J | ν ω ν Ν | 3 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 |
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| H20919 H42553 | VA733056 V16654 | 116156 | T49928 | 124541 | 2 | W67931 | AA139263 | HSII69180 | ω | AA215625 | R46751 | 250026 | | w | н39899 | A059314 | | AF034173 | 130 | AA171296 | 52 | A141415 | AF034173 | AA165945 | AA048742 | 5314 | 2000 |
| yn65b09.rl yo63b10.rl | | ٠. | | • ~ | mh49e03.r1 | zd38g09.r1 | 6.r | Human DRES | 3.6 | | yj54a01.s1 | yj59e07.r1 | | CO | yp02h01.s1 | zf66b05.s1 | 'n | sapi | | н | 'n. | 709.5p | pie | | • | mr87g02.rl | • |
| sapie | es f | Sap | Homo sapien | Homo sapien | | _ | Soares 2NbM | 30 mRNA sea | rime LD Dros | NCI_CGAP_GC | Homo sapien | Homo sapien | Homo sapien | | api | Soares reti | omo sapi | on2 c | Tech | ര | Soares | CÍN. | ns ntcon2 c | | Soares mous | | Barstead mo |
| 5.30e-10 5.30e-10 | .30e | .30e | .40e | .40e | .40e | .30e | 40e | 500 | 1.02e | 1.02e | 4.08e | 1.02e | 4.08e | .02e | .54e | .08e | .08e | .87e | .87e | .51e | .08e | . 08e | .60e | . 60e | . 60e | .60e | . aye |

ALIGNMENTS

| TITLE | AUTHORS | REFERENCE | | | | ORGANISM | SOURCE | KEYWORDS | NID | ACCESSION | | | | | | DEFINITION | RESULT 1 LOCUS |
|---|--|--------------------|----------------------------|---|--|-------------------------|------------|----------|----------|-----------|----------------|---|--|--|--|---|--------------------------------------|
| Brokstein, P., Lewis, S. and Rubin, G.M. BDGP/HHMI Drosophila EST Project | Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., | 1 (bases 1 to 442) | Drosophilidae; Drosophila. | Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; | Eukaryotae; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; | Drosophila melanogaster | fruit fly. | EST. | 92285254 | AA538738 | mRNA sequence. | D.melanogaster Dl mRNA for delta protein, involved in neurogenesis, | EGF-like repeats (EGF- epidermal growth factor); Y00222: | X05140: Drosophila melanogaster mRNA fragment of Dl locus with | Drosophila melanogaster cDNA clone LD18334 5prime similar to | LD18334.5prime LD Drosophila melanogaster embryo BlueScript | AA538738 442 bp mRNA EST 19-JAN-1998 |

JOURNAL COMMENT

Unpublished (1997)

Contact: Harvey, D.

G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: httpd://fruitfly.berkeley.edu/EST, est@fruitfly.berkeley.edu
Plate: 183 row: C column: 10
High quality sequence stop: 390.

Location/Qualifiers

FEATURES

source

/organism="Drosophila melanogaster"
/note="Organ: embryo; Vector: BlueScript SK; Site_1:
ECORI; Site_2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis kit. Oligo dT-primed and directionally cloned at
ECORI and XhoI in BlueScript SK(+/-)"

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Contact: Harvey, D.
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1 (bases 1 to 379)
Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein, P., Lewis, S. and Rubin, G.M.

Uppublished (1997)
                                                                                                                                                                                                                                                                           61 CGCCAACGGCTGGAGCGGAAAGATGTGCGAGGAGAAAGTGCTCACGTGTTCGGACAAACC 120
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                                                                                                                                                       Length 442;
                                                                                                                                                      Score 436; DB 13;
Pred. No. 0.00e+00;
0; Mismatches 3
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M. Rubin-Molecular and Cell Biology
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Drosophila melanogaster
                                                                                                                                                      Query Match 15.1%;
Best Local Similarity 99.3%;
Matches 439; Conservative
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1. 379
/organism="Drosophila melanogaster"
/organism="Drosophila melanogaster"
/organism="Drosophila melanogaster"
/organism="Drosophila melanogaster"
/organism="Drosophila melanogaster"
/organism="Site_1: Who; Constructed using Stratagene ZAP-cDNA Synthesis Kit. Oligo dr-primed and directionally cloned at EcoRI and XhoI in BlueScript SK(+/-)"
/db_xref="Brosophila melanogaster embryo BlueScript"
/clone_lib="LD Drosophila melanogaster embryo BlueScript"
/sex="male and female"
/dev_stage="O to 24 hours mixed stage embryonic"
/lab_host="SOLR"
Email: httpd://fruitfly.berkeley.edu/EST, est@fruitfly.berkeley.edu
Plate: 195 row: G column: 12
High quality sequence stop: 182.
Location/Qualifiers
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Pteryyota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein, P., Lewis, S. and Rubin, G.M. BDGP/HHMI Drosophila EST Project Unpublished (1997)
Other_ESTs: CK00091.5prime.contig
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Local Similarity 99.7%;
nes 378; Conservative
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TITLE
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Best Local Similarity 97.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                        Marra,M., Hillier,L., Allen,M., Bowles,M., Districh,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
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Contact: Marra M/Mouse EST Project
                                                                                Unpublished (1996)
                                                                                                                            Waterston,R.
The WashU-HHMI Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g1476296
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nouse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 567)
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/note="Organ: embryo; Vector: Bluescript SK; Site_1: ClaI;
Site_2: PstI; mRNA purified from rough endoplasmic
reticulum-bound polysomes was used as a template. cDNA's
directionally cloned at HinDIII and PstI in Bluescript
SKt. Cloned into HinDIII, but the site was destroyed to
add an adapter sequence. So ClaI is now the restriction
enzyme at site I of vector: Primers - 5' universal, 3'
ml3-20 (reverse), 3' T3, 5' T7."
/db_xref="BDGP_EST:BDCln000089"
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/sex="male and female"
/dev_stage="0 to 24 hours old embryo"
/lab_host="XLI Blue MRF"
126 c 97 g 180 t 9 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:7227"
/clone="CK00091"
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Pred. No. 2.05e-235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                     1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1117 CACCACTGTATCCTGGAGCGCATTTGCATGTGTACAATCCCTCGCCGGTGTTGAAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                353
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                                                                                                                                                                                                                                                                                                             937
                                                                                                                                                                                                                                                                                                                                          473
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Local Similarity 68.8%;
                                                                                                                                                                                                                                                                                                                                       AACCTGGGTATCGGATGCACTCATCGCA 500
                                                                                                                                                                                                                                                                                                                                                                       GGCCCCCCAGCCTTCCTGGCAGTTACACTGCCTAGGTTGCTGGCAGGTGCCATGGAGAC 472
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                                                                                                                                                                                                                                                                                                             AGTTCGGTTCCAGAACGCACTCGTTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143;
                                                                                                                                                   rice.
                                                                                                                                                                                                 cDNA clone 97SN1787, mRNA sequence. AA754459
                                                                                                                                                                                                                                AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Large-scale Sequencing Analysis Unpublished (1998)
                            Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., St Lee, M.C. and Eun, M.Y.
                                                                                        Eukaryotae; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Poales; Poaceae; Oryza.
                                                                                                                                       Oryza sativa
                                                                                                                                                                                     g2801165
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28M13 rev2 from Amersham
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                                                                       (bases 1 to 252)
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/lab_host="DH10B"
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162 c
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0; Mismatches 65;
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Pred. No. 5.84e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 567;
                 from Rice Immature Seed
                                            Sohn, U.I., Kang, K.Y.,
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Oryza sativa
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JOURNAL
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                                                                                                                                                                                                                                                                                   /cultivar="Milyang33"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/Note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/Not: Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:430"
/clone="97SN1787"
/clone="97SN1787"
/tissue_type="Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="8" days after pollination"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA754458 247 bp mRNA EST 20-JAN-1998 97SM1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1784, mRNA sequence.
AA754458 92801164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

1 (bases 1 to 247)

Nahm, B. H., Kim, J. K., Cheong, J. J., Kim, S. I., Hahn, T. R., Moon, E. P., Kim, W. T., Kim, W. Y., Yang, M. S., Park, R. D., Sohn, U. I., Kang, K. Y., Lee, M. C. and Eun, M. Y.
                                Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
National Inst. of Agri. Sci. and Tech, RDA
Way, Yungqido, Korea
Tel: 82 331 290 0307
Fax: 82 331 290 0307
Fax: 82 391 290 0307
Fax: 82 391 290 0307
Fax: 82 391 290 0307
For Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2632 GAGTGCCGCAGACCACGGATCGCTGCTGTTGCGCCGTCCCCGCTCCGCTGCCG 2573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 BVBNTKVDVGNHTRCSRWRBVTRWAHYHDYTNCBBYNNNDYHWWHBBMYBBTGCMTCTMW 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 CWBHYNTKCT-ASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 SYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTW-GTVNWBNVSGDWHYW 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Natch 2.1%; Score 60; DB 13; Length 252 Local Similarity 10.1%; Pred. No. 6.76e-60; es 23; Conservative 117; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 TRSYTCVRKYCVMWMTKKVVKKYHVVBBGCHBTDSKCKTMWMTNKHV 246
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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    .252
    /organism="Oryza sativa"

                                                                                                                                                                                                                                 Location/Qualifiers
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1. .247
/organism="Oryza sativa"
/organism="Oryza sativa"
/oultivar="Milyang23"
/oultivar="Milyang23"
/oultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhof: Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
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/clone="97SN7784"
/clone="97SN7784"
/clone="97SN7784"
/clone="15-Race Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E: coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.
AA754459 92801165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Boalos; Poaceae; Oryza.

1 (bases 1 to 252)

1 (bases 1 to 252)

1 (bases 1 to 252)

1 Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,

Lee, M.C. and Eun, M.Y.
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University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: Mi3 Reverse Primer.
Location/Qualifiers
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 49-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 VDINTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBTAYCDYBHYBDRANHVDDTRCTNDRG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 YCNYTASDNGTSATKRVTGYDKTDSDCGGGCWRKVTYGSSBYBRCGVNVMVRTTSMWTDK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 MTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHCRYTVB-WYYARSKYGYGTBYYSWN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.0%; Score 57; DB 13; Length 247 Best Local Similarity 12.1%; Pred. No. 1.40e-54; Matches 24; Conservative 101; Mismatches 72; Indels
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Email: myeun@sun20.asti.re.kr
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                                                                                                                       Location/Qualifiers
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TITLE
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Best Local Similarity 11.7%;
Matches 25; Conservative
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                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CVRKYCVMWMTKKVVKKYHVVBBGCHBTDSKCKT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTAGTAGCAAAGTTGACTTGTGCCTCATC-AGACCGTGTGCCAATGGAGGAACCTGCTT 1661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA051023 570 bp mRNA EST 09-SEP-1996 mg73f08 rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 438663 5' similar to gb:X80903 M.musculus mRNA for Delta-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 570)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                 WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 protein (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                        Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
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                                                                                                                                                     primer: -28M13 rev2 from Amersham
                                                                                                   quality sequence stop: 287
Location/Qualifiers
                                                                                                                                                                                                      clone is available royalty-free through LLNL; E Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                  314 286 1800
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                    /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 others
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pT7T3D-Pac
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  (Pharmacia) with a modified
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 GCCTTTGCGCCTGCAGGACCTTCTTTCGCGTATGCCTCAAGCACTACCAGGCCAGCGTGT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 66.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGCCTGCCTGATGGCC-GCAGATC--GAACCCGC-CTTCAGCAACCCCATCCGATTCC 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTCTCGTTCTCATGGCCGGGTACCTTCTCGCTGATCGTCGAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAATCTGACCGACGCCCAGCGCTTCCAGAACAAGGGCTTCACGAATCCCATCCAGTTCC
                                                                              Department of Cytogenetics
National Inst. of Agri Sci.
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
          Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seg primer: M13 Reverse Primer.
                                                                                                                                                                    Contact: Eun M.Y.
                                                                                                                                                                                                     Large-scale Sequencing Analysis Unpublished (1998)
                                                                                                                                                                                                                                    1 (bases 1 to 247)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., S
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                      Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; L
                                                                                                                                                                                                                                                                                                                                                         Oryza sativa
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97SN1784 Rice
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Location/Qualifiers
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/dev_stage="13.5-14.5dpc
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                           97SN1784, mRNA sequence.
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180 c
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Pred. No. 4.48e-51
0; Mismatches 7
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RESULT

SOURCE KEYWORDS

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ORIGIN

FEATURES

COMMENT

TITLE

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 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zf14hl1.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 376965 5' similar to PIR:A56136 A56136 jagged protein precursor rat ;, mRNA sequence.
AA046860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 1482 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/note="Organ: heart; Vector: p17T3D (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 GGACTCGGACGGACGGCCAAGTGCCTGGGCAGCTGCAAGA-CGCGGTTTCGCGTCT 343
                                                                                                                                                                                                                                                                                                                                                                              77 YGTBYYSWNVDINIGGIGVGKTIVNVHSGWNNRCSNSVVYVWBIAYCDYBHYBDRANHVD 136
                                                                                                                                                                                                                                                                                                                                                                                                226 CG-CCTGAAGTACTTCAGCAACGATCACGGCGGGACAACGAGGGTCGCTGCTGCAGCGG 284
                                                                                                                                                                                                                                                                                                                                            167 CAGCATTCATTTGCTTCACAGTCATCGTGCAGGTTCACA-GTTCCGGCAGCTTTGAGTTG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                137 DTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDSDCGGGCWRKVTYGSSBYBRCGVNVMV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens

Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Bukaryotae; Butheria; Primates; Catarrhin1; Hominidae; Homo.

(bases 1 to 602)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rikin, L., Rohlfing, T., Tan, F., Trevaskis, E.,

Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

Wash Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                          BAMMNKHTHMMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHCRYTVBWYYARSKYG 76
                                                                                                                                                                                                                                                                            Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                        Length 247;
                                                                                                                                                                                                                                          Score 51; DB 13; Length 247
Pred. No. 3.60e-44;
108; Mismatches 78; Indels
/organism="Oryza sativa"
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WashU-Merck EST Project
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|larity 10.4%;
|Conservative 1
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Best Local Similarity 1
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Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 ATCTTTGTCACAGAGCTGGCCGCCCCAGTTGGTCTCACAGAGGCACTGCCAGGGCTCATT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                839 TIGGCG-CATTIGGGTATGTGACAGTAATCGCCCTGCCATCGGGTCAAACAGATAATTIC 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 GCCATTCTGGTCACAGGCATAGTGTCCAAAGAAGTCATCTCTGGGGCGGCAGAACTTATT 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 ACAGATGCCGTGGACGCATCCCGGGTGTGCGATGCACTTATCACAGTACAGGCCTTGCCA
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9
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                                                                                                                                                                                                                                                                                                                                     Length 602;
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                                                                                                                                                                                            /clone="376965"
/clone_lib="Soares fetal heart NbHH19W"
                                                                                                                                                                                                                                                                                                                                    Score 51; DB 23; Lei
Pred. No. 3.60e-44;
0; Mismatches 159;
                                                                                                                                                                                                                         /sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin
                                                                                                                                                                                                                                                                                      145 t
                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                      158 g
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Local Similarity 59.9%;
es 246; Conservative
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Best Local Similarity 73.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                      WashIngton University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                          Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 445)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub.
Marra, M., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vo68b02.rl
1055019 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
High quality sequence stops: 323
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                     Unpublished (1996)
                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
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WashU-Merck EST Project
Washington University School of Medicine
                                            Email: mouseest@watson.wustl.edu
                                                                                                                                                                        Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                               Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia;
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse
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/clone="30502"
118 c 102 g 8
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Pred. No. 1.82e-42;
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Best Local Similarity 70.6%;
Matches 72; Conservative
                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 TTCTGCCGGCCCCGCAACGACTTCTTTGGCCACTATACCTGC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    667 CTGGAGTACGATTTCCGTGTCACCTGCGATCTCAACTACTACGGATCCGGCTGTGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 CTGGAGCTGCAGATCCGAGTGCGCTGTGATGAGAACTACTACAGTGCCACCTGCAACAAG 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCTGCCGGCCCCGCGACGATTCATTTGGACACTCGACTTGC
                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:275988
                                                                                                                              Contact: Marra M/Mouse EST Project
Washir-HHMI Mouse EST Project
Washirgton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mh99e03.rl Soares mouse clone 459100 5' similar
                                                                                              Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                              Waterston, R.
The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor
AA024229
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                      Theising, B., Wylie, T.,
                                                                                                                                                                                                                                                                                                                                                                                    Mus
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             þ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="mammary gland"
/dev_stage="4 weeks"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="1055019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares mouse mammary gland NbMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
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                                                                                                                                                                                                                                (1996)
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Pred. No. 2.96e-29;
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AA153148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
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                                         Marray. Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Marray. Hillier,L., Allen,M., Bowles,M., Martin,J., Morris,M., Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA238559 589 bp mRNA EST 03-MAR-1997 my35e01.rl Barstead mouse pooled organs MPLRB4 Mus musculus CDNA clone 697848 5' similar to gb:U15980 Mus musculus (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGGTATAGTGGCCAAAGAAGTCGTTGCGGGGCCGGCAGAACTTGTTGCAGGTGGCACT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           768 GCAAGTCGAGTGTCCCAAATGAATCGTCGCGGGGCCGCAGAACTTGGCACAGCCGGATCC 709
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                                                                                                                                                                                                                                                                                                                                                                                 Length 485;
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Pred. No. 2.96e-29;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAGTAGTICTCATCACAGCGTACTCGGATCTGCAGCTCCAG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        708 GTAGTAGTTGAGATCGCAGGTGACACGGAAATCGTACTCCAG 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -28ml3 rev2 ET from Amersham
Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 447. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        94
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Best Local Similarity 70.6%;
Matches 72; Conservative
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149 c
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91862583
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AUTHORS
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JOURNAL
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA153148 592 bp mRNA EST 11-FEB-1997 mr87902.rl Stratagene mouse heart (#937316) Mus musculus cDNA clone 604466 5' similar to gb:U15980 Mus musculus (MOUSE);, mRNA
                                      'n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1091 GCAAATGCGCTCCAGGATACAGTGGTGATGATTGCGAAAATGAGATCTACTCCTGCGATG 1150
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851 ATGGACATTGCGACAAACCCAATGAATGCGTTTGCCAACTGGGCTGGAAGGGAGCCTTGT 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 -- CA-ACCCCCTGCGCCCAACATGGAACTTGCGTGGACCTGGAGAAAGGCCCAGTACGAAT 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 ATGGATTCTGCGAGGCTGACAATGTCTGCAGGTGCCATGTTGGCTGGGAGGGTCCCCTCT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                              /clone_lib="Barstead mouse pooled organs MPLRB4"
/sex="mixed"
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Pred. No. 1.89e-21
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/organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                 174 g
                                                                                                                                                                                                                                                                                                                         /dev_stage="7 day"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.3%;
Best Local Similarity 58.3%;
Matches 200; Conservative
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a 179 c
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mRNA
BASE COUNT
ORIGIN
Search completed: Sat Jun 13 09:56:28 1998 Job time: 4728 secs.
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Best Local Similarity 63.8%;
Matches 90; Conservative
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                                                                 299 GTGACAAGTGTGTAACTGCCCCTGGCTGTGTCAATGGAGTCTGCAAGGAACCATGGCAGT 358
                                                                                                                                911 GCAACGAGTGCGTTCTGGAACCGAACTGCATCCATGGCACCTGCAACAAACCCTGGACTT 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:369898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 381.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                   106 a
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Stratagene mouse heart (#937316)"
/sex="pooled"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
<1. .>592
196 c 176 g 114 t
                                                                                                                                                                                                                                                               Score 39; DB 23; Length 592 Pred. No. 1.60e-24; 0; Mismatches 51; Indels
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118184969 CA: 118(19)184969g **JOURNAL** Mouse mammary tumor gene int-3: a member of the notch gene family transforms mammary epithelial cells AUTHOR(S): Robbins, Joan; Blondel, Bruno J.; Gallahan, Daniel; Callahan, Robert LOCATION: Lab. Tumor Immunol. Biol., Natl. Cancer Inst., Bethesda, MD, 20892, USA JOURNAL: J. Virol. DATE: 1992 VOLUME: 66 NUMBER: 4 PAGES: 2594-9 CODEN: JOVIAM ISSN: 0022-538X LANGUAGE: English SECTION: CA203004 Biochemical Genetics CA213XXX Mammalian Biochemistry IDENTIFIERS: mouse mammary tumor gene int3 transformation, epithelium transformation mouse notch like gene DESCRIPTORS: Epithelium... cell, of mammary gland of mouse, gene int-3 transformation of Deoxyribonucleic acid sequences... for gene int-3 protein of mouse mammary tumor Proteins, specific or class, gene int-3... gene for, of mouse mammary tumor, sequence of and epithelial cell transformation by Virus, animal, murine mammary tumor... gene int-3 integration site for, sequence of and epithelial cell transformation by gene int-3 of mammary tumor of, sequence of and epithelial cell transformation by Gene, animal, Notch... mouse mammary tumor gene int-3 like, of Drosophila melanogaster, sequence of and epithelial cell transformation by Mammary gland, neoplasm... notch family gene int-3 of mouse, sequence of and epithelial cell transformation by Drosophila melanogaster... notch gene of, mouse mammary tumor gene int-3 as member of family of, sequence of and epithelial cell transformation by Protein sequences... of gene int-3 protein, of mouse mammary tumor Gene, animal, int-3... of mouse mammary tumor, sequence of and epithelial cell transformation Deoxyribonucleic acids, repetitive... Saccharomyces cerevisiae cell cycle gene cdc-10 homolog, in gene int-3 of mouse mammary tumor CAS REGISTRY NUMBERS: 146991-60-8 amino acid sequence of, complete 139861-79-3 nucleotide sequence of 16/7/176 (Item 3 from file: 399)

DISSERTATION

DIALOG(R) File 399:CA SEARCH(R)

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TAN-1, the human homolog of Drosophila "Notch", is involved in

chromosomal translocations in human lymphoblastic neoplasma

CA: 120(11)130975d

AUTHOR(S): Ellisen, Leif William

LOCATION: Stanford Univ., Stanford, CA, USA

DATE: 1992 PAGES: 80 pp. CODEN: DABBBA LANGUAGE: English CITATION: Diss. Abstr. Int. B 1993, 53(7), 3307 AVAIL: Univ. Microfilms Int., Order No. DA9234046

SECTION:

CA214001 Mammalian Pathological Biochemistry

CA203XXX Biochemical Genetics

IDENTIFIERS: gene TAN1 chromosome translocation lymphoblastic leukemia DESCRIPTORS:

Leukemia, T-cell acute lymphocytic...

gene TAN-1 translocation in, in human

Recombination, genetic, translocation...

of gene TAN-1, in human T-cell acute lymphoblastic leukemia

Gene, animal...

TAN-1, chromosomal translocation of, in human T-cell lymphoblastic leukemia

Chromosome, human 7...

TAN-1 gene translocation from, in human T-cell lymphoblastic leukemia

16/7/141 (Item 28 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 1996 Knight-Ridder Info. All rts. reserv.

06701790 89003790

Expression of the differentiation antigen F7D6 in tumorous tissues of Drosophila.

Bedian V; Jungklaus CE

Department of Biology, Clarkson University, Potsdam, New York 13676.

Dev Genet (UNITED STATES) 1987, 8 (3) p165-77, ISSN 0192-253X

Journal Code: DEG Languages: ENGLISH

Document type: JOURNAL ARTICLE

The 63-kDa antigen recognized by the monoclonal antibody F7D6 is present all Drosophila embryonic cells and disappears from most tissues as each one reaches its final, differentiated state. Larval tissues lose the antigen around the time of hatching, imaginal tissues lose it during metamorphosis, and germ cells lose it during gametogenesis (Bedian et al: Devel Biol 115:105-118, 1986). The nervous system and spontaneously contracting musculature of the gut and gonads are exceptions and remain antigen positive at all stages. The F7D6 antigen appears to be associated with dividing, undifferentiated cells and electrogenic cells. This prompted us to test tumors for antigen presence. We tested four different recessive mutants that give rise to four different types of tumorous transformation: the embryonic tumor Notch, several larval melanotic tumors, the imaginal disc tumor 1(2)gl, and three alleles of the ovarian tumor otu. In all cases, tumorous tissues in homozygotes contained the F7D6 antigen. The electrophoretic mobility of the antigen appeared to be unaltered in tumorous tissues compared to normal cells, but the antigen is expressed at higher levels. The antigen is found on the cytoplasmic surface of plasma membranes and appears to be a marker of undifferentiated normal and tumorous cells. Similarities and differences between the F7D6 antigen and Drosophila c-src protein are discussed.

16/7/139 (Item 26 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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06969982 89271982

[Adult T-cell leukemia (ATL)]

Takatsuki K

Kumamoto University Medical School.

Gan To Kagaku Ryoho (JAPAN) Apr 1989, 16 (4 Pt 2-1) p880-5, ISSN 0385-0684 Journal Code: 6T8

Languages: JAPANESE Summary Languages: ENGLISH Document type: JOURNAL ARTICLE English Abstract

Adult T-cell leukemia (ATL) was first discovered and reported in Japan, where it has a high incidence in the southwest region. The retrovirus HTLV-I (human T-cell lymphotropic virus type I) is considered to be related to its etiology. In ATL endemic areas, HTLV-I carriers are found at a fairly high percentage even among healthy individuals. ATL shows diverse clinical features. It can be divided into 5 types (acute type, chronic type, smoldering type, crisis type, and lymphoma type). ATL cells originate from the CD4-positive subset of peripheral T cells; they show a characteristic notch in the nucleus and a lobulation tendency. ATL resists chemotherapy, and patients with acute and lymphoma types have quite a poor

prognosis. A definite diagnosis of ATL is made by documenting the presence of HTLV-I proviral DNA in the DNA of tumor cells. HTLV-I infection is caused by transmission of live lymphocytes via three routes (from mother to children, from males to females, and by transfusion). Familial occurrence of ATL is frequently seen. HTLV-I infection is also seen in other countries, but its incidence is highest in Japan. It is thus an urgent task for Japanese physicians to eliminate HTLV-I infection.

16/7/128 (Item 15 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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08122975 92260975

Cancer, chromosomes, and genes.

Nowell PC

Department of Pathology and Laboratory Medicine, University of Pennsylvania, School of Medicine, Philadelphia.

Lab Invest (UNITED STATES) Apr 1992, 66 (4) p407-17, ISSN 0023-6837

Journal Code: KZ4

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW; REVIEW, ACADEMIC

(67 Refs.)

16/7/123 (Item 10 from file: 155) DIALOG(R) File 155:MEDLINE(R)

(c) format only 1996 Knight-Ridder Info. All rts. reserv.

09041700 94356700

Analysis of phenotypic abnormalities and cell fate changes caused by dominant activated and dominant negative forms of the Notch receptor in Drosophila development.

Rebay I; Fortini ME; Artavanis-Tsakonas S

Howard Hughes Medical Institute, Department of Cell Biology, Yale University, New Haven, Connecticut 06536-0812.

C R Acad Sci III (FRANCE) Sep 1993, 316 (9) p1097-123, ISSN 0764-4469 Journal Code: CA1

Languages: ENGLISH, FRENCH

Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL

The Notch gene of Drosophila plays an important role in cell fate specification throughout development. The Notch protein contains a large extracellular domain of 36 EGF-like repeats as well as 3 Notch/lin-12 repeats and an intracellular domain with 6 cdc10/ankyrin repeats, motifs which are highly conserved in several vertebrate Notch homologues [1-7]. In this review we summarize the results of two recent studies which attempt to establish structure-function relationships of the various domains of the Notch gene product [8, 9]. The functions of various structural domains of the Notch protein in vivo were investigated using a series of deletion mutants which have been ectopically expressed either under the hsp70 under the sevenless eye-specific promoter. heat-shock promoter orTruncation of the extracellular domain of Drosophila Notch produces an activated receptor as judged by its ability to cause phenotypes matching those of gain-of-function alleles or duplications of the Notch locus [8]. Equivalent truncations of vertebrate Notch-related proteins have been associated with malignant neoplasms and other developmental abnormalities 10, 11]. In contrast, dominant negative phenotypes result from overexpression of a protein lacking most intracellular sequences. These

results were extended by an analysis of activated Notch function at single-cell resolution in the Drosophila compound eye [9]. It was shown that while overexpression of full-length Notch in defined cell types has no apparent effects, overexpression of activated Notch in the same cells transiently blocks their proper cell-fate commitment, causing them to either adopt incorrect cell fates or to differentiate incompletely. Moreover, an activated Notch protein lacking the transmembrane domain is translocated to the nucleus, raising the possibility that Notch may participate directly in nuclear events. (68 Refs.)

16/7/116 (Item 3 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
(c) format only 1996 Knight-Ridder Info All rts

(c) format only 1996 Knight-Ridder Info. All rts. reserv.

09600265 96121865

Oncogene activation and oncogene cooperation in MMTV-induced mouse mammary cancer.

van Leeuwen F; Nusse R

Howard Hughes Medical Institute, Department of Developmental Biology, Beckman Center, Stanford University, Medical Center, CA 94305-5428, USA.

Semin Cancer Biol (UNITED STATES) Jun 1995, 6 (3) p127-33, ISSN 1044-579X Journal Code: A6Y

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL

In this short review, we will give an overview of the various genes that can be activated by insertion of proviral DNA of the mouse mammary tumor virus during the formation of mammary cancer. These genes fall within three families: Wnt genes, FGF genes and Notch-related genes. We will summarize our current understanding of the roles of these genes in tumorigenesis and in normal development, and the mechanisms of action of their gene products. Finally, we will give some examples of cooperation between these genes in various biological settings. (91 Refs.)

16/7/113 (Item 6 from file: 144) DIALOG(R) File 144: Pascal (c) 1996 INIST/CNRS. All rts. reserv.

04166645 PASCAL No.: 75-0002761

DEVELOPMENTAL CAPACITIES OF BENIGN AND MALIGNANT NEOPLASMS OF DROSOPHILA GATEFF E; SCHNEIDERMAN H A

CENT. PATHOBIOL., UNIV. CALIFORNIA, IRVINE, CALIF. 92664, USA

Journal: ARCH. (WILHELM ROUX) ENTWICKL.-MECH. ORG., 1974, 176 (1) 23-65 Availability: CNRS-3573

No. of Refs.: 4P.1/2

Document Type: P (SERIAL) ; A (ANALYTIC)

Country of Publication: FEDERAL REPUBLIC OF GERMANY

Language: ENGLISH Summary Language: GERMAN

16/7/112 (Item 5 from file: 144) DIALOG(R) File 144: Pascal (c) 1996 INIST/CNRS. All rts. reserv.

10278296 PASCAL No.: 92-0484208

Expression pattern of Motch, a mouse homolog of Drosophila notch, suggests an important role in early postimplantation mouse development

DEL AMO F F; SMITH D E; SWIATEK P J; GENDRON-MAGUIRE M; GREENSPAN R J; MCMAHON A P; GRIDLEY T

Roche inst. molecular biology, dep. cell developmental biology, Nutley NJ 07110, USA

Journal: Development: (Cambridge), 1992, 115 (3) 737-744 ISSN: 0950-1991 Availability: INIST-7560; 354000020190410090

No. of Refs.: 1 p.1/2

Document Type: P (Serial) ; A (Analytic) Country of Publication: United Kingdom

Language: English

The Notch gene of Drosophila encodes a large transmembrane protein involved in cell-cell interactions and cell fate decisions in the Drosophila embryo. To determine if a gene homologous to Drosophila Notch playis a role in early mouse development, we screened a mouse embryo cDNA library with probes from the Xenopus Notch homolog, Xotch. A partial cDNA clone encoding the mouse Notch homolg, which we have termed Motch, was used to analyze expression of the Motch gene. Motch transcripts were detected in a wide variety of adult tissues, which included derivatives of all three germ layers

16/7/110 (Item 3 from file: 144) DIALOG(R) File 144: Pascal (c) 1996 INIST/CNRS. All rts. reserv.

12471360 PASCAL No.: 96-0134151

Epithelial expression and chromosomal location of human TLE genes : implications for notch signaling and neoplasia

YANLING LIU; GHASSAN DEHNI; PURCELL K J; SOKOLOW J; CARCANGIU M L; ARTAVANIS-TSAKONAS S; STIFANI S

McGill univ., Montreal neurological inst., Montreal PQ H3A 2B4, Canada Journal: Genomics: (San Diego, CA), 1996, 31 (1) 58-64

ISSN: 0888-7543 Availability: INIST-21389; 354000052959520080

No. of Refs.: 26 ref.

Document Type: P (Serial) ; A (Analytic)

Country of Publication: USA

Language: English

The TLE genes are the human homologues of Drosophila groucho, a member of the Notch signaling pathway. This pathway controls a number of different cell-fate choices in invertebrates and vertebrates. We are interested in investigating the functions of the TLE gene family during epithelial determination and carcinogenesis. We show that expression of individual TLE genes correlates with immature epithelial cells that are progressing toward their terminally differentiated state, suggesting a role during epithelial differentiation. In both normal tissues and conditions resulting from incorrect or incomplete maturation events, such as metaplastic and neoplastic transformations, TLE expression is elevated and coincides with Notch expression, implicating these molecules in the maintenance of the undifferentiated state in epithelial cells. We also show that TLE1 and TLE2 are organized in a tandem array at chromosomal location 19p13.3, while TLE3 maps to 15q22.

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16/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

13041777 BIOSIS Number: 99041777

Exclusive development of T cell neoplasms in mice transplanted with bone marrow expressing activated Notch alleles

Pear W S; Aster J C; Scott M L; Hasserjian R P; Soffer B; Sklar J; Baltimore D

Massachusetts Inst. Technol., Room 68-380, 77 Massachusetts Ave., Cambridge, MA 02139-4307, USA

Journal of Experimental Medicine 183 (5). 1996. 2283-2291.

Full Journal Title: Journal of Experimental Medicine

ISSN: 0022-1007 Language: ENGLISH

Print Number: Biological Abstracts Vol. 102 Iss. 002 Ref. 023950

Notch is a highly conserved transmembrane protein that is involved in fate decisions and is found in organisms ranging from Drosophila to cell humans. A human homologue of Notch, TAN1, was initially identified at the breakpoint chromosomal of a subset of T-cell lymphoblastic leukemias/lymphomas containing a t(7;9) chromosomal translocation; however, oncogenesis has been unclear. Using a bone marrow in reconstitution assay with cells containing retrovitally transduced TAN1 analyzed the oncogenic potential of both nuclear extranuclear forms of truncated TAN1 in hematopoietic cells. Although the Moloney leukemia virus long terminal repeat drives expression in most hematopoietic cell types, retroviruses encoding either form of the TAN1 protein induced clonal leukemias of exclusively immature T cell phenotypes in apprx 50% of transplanted animals. All tumors overexpressed truncated TAN1 of the size and subcellular localization predicted from the structure of the gene. These results show that TAN1 is an oncoprotein and suggest truncation that overexpression are important determinants of and transforming activity. Moreover, the murine tumors caused by TAN1 in the bone marrow transplant model are very similar to the TAN1-associated human tumors and suggest that TAN1 may be specifically oncotropic for T cells.

16/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

13034202 BIOSIS Number: 99034202

T cell leukemia-associated human notch-translocation-associated notch homologue has I-kappa-B-like activity and physically interacts with nuclear factor-kappa-B proteins in T cells

Guan E; Wang J; Laborda J; Norcross M; Baeuerle P A; Hoffman T Lab. Cell Biol., Div. Monoclonal Antibodies, Cent. Biologics Eval. Res., Federal Drug Administration, Building 29B, Room 4G03, HFM558, 8800 Rockville Pike, Bethesda, MD 20892, USA

Journal of Experimental Medicine 183 (5). 1996. 2025-2032.

Full Journal Title: Journal of Experimental Medicine

ISSN: 0022-1007 Language: ENGLISH

Print Number: Biological Abstracts Vol. 102 Iss. 002 Ref. 016375

Translocation-associated Notch homologue (TAN-1), a gene originally cloned from the translocation breakpoint of a human T cell leukemia carrying a 9:7(q34.3) translocation, encodes a protein belonging to the Notch/Lin-12/Glp-1 receptor family. These receptors mediate the specification of numerous cell fates during development in invertebrates and vertebrates. The intracellular portion of Notch/TAN-1 contains six ankyrin repeats that are similar to those found in cytoplasmic I-kappa-B

proteins. I-kappa-B proteins are specific inhibitors of nuclear factor (NF)-kappa-B/Rel transcription factors. Here we show that TAN-1 has functional properties of an I-kappa-B-like regulator with specificity for the NF-kappa-B p50 subunit. A recombinant polypeptide corresponding to the cytoplasmic portion of TAN-1 (TAN-1-C) specifically inhibited the DNA binding of p50-containing NF-kappa-B complexes. When overexpressed in an appropriate cell line, TAN-1-C prevented kappa-B-dependent transactivation in transient reporter gene assays in a fashion similar to the structurally related protein, Bcl-3. TAN-1-C could activate kappa-B-dependent gene expression by attenuating the inhibitory effect of an excess of p50 homodimers. Immunoprecipitation experiments showed that the TAN-1 from a T cell line is associated with NF-kappa-B containing p50 and p65 subunits. These observations indicate that TAN-1-C may directly engage NF-kappa-B transcription factors and modulate nuclear gene expression.

16/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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12098006 BIOSIS Number: 98698006

Epithelial expression and chromosomal location of human TLE genes: Implications for notch signaling and neoplasia

Liu Y; Dehni G; Purcell K J; Sokolow J; Carcangiu M L; Artavanis-Tsakonas S; Stifani S

Montreal Neurol. Inst., 3801 University St., Montreal, PQ H3A 2B4, Canada Genomics 31 (1). 1996. 58-64.

Full Journal Title: Genomics

ISSN: 0888-7543 Language: ENGLISH

Print Number: Biological Abstracts Vol. 101 Iss. 007 Ref. 098287

The TLE genes are the human homologues of Drosophila groucho, a member of the Notch signaling pathway. This pathway controls a number of different gene family during epithelial determination and carcinogenesis. We show that expression of individual TLE genes correlates with immature epithelial cells that are progressing toward their terminally differentiated state, suggesting a role during epithelial differentiation. In both normal tissues and conditions resulting from incorrect or incomplete maturation events, such as metaplastic and neoplastic transformations, TLE expression is elevated and coincides with Notch expression, implicating these molecules in the maintenance of the undifferentiated state in epithelial cells. We also show that TLE1 and TLE2 are organized in a tandem array at chromosomal location 19p13.3, while TLE3 maps to 15q22.

16/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

11799009 BIOSIS Number: 98399009

TAN-1, human homolog of Drosophila Notch, encodes a IKB-like activity
Guan E; Wang J H; Laborda J; Lizzio E; Norcross M; Baeuerle P A; Hoffman

Cent. Biol. Eval. Res., US FDA, Freiburg, Germany 0 (0). 1995. 693.

Full Journal Title: 9TH INTERNATIONAL CONGRESS OF IMMUNOLOGY. The 9th International Congress of Immunology; Meeting Sponsored by the American Association of Immunologists and the International Union of Immunological

Societies, San Francisco, California, USA, July 23-29, 1995. ix+742p. 9th International Congress of Immunology: San Francisco, California, USA.

ISSN: ********
Language: ENGLISH

Print Number: Biological Abstracts/RRM Vol. 047 Iss. 009 Ref. 161412

16/7/10 (Item 10 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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11789761 BIOSIS Number: 98389761

Functional analysis of the TAN-1 gene, a human homolog of Drosophila

Aster J; Pear W; Hasserjian R; Erba H; Davi F; Luo B; Scott M; Baltimore D: Sklar J

Div. Molecular Oncol., Dep. Pathol., Brigham and Women's Hosp., Harv. Med. Sch., Boston, MA 02115, USA

0 (0). 1994. 125-136.

Full Journal Title: COLD SPRING HARBOR LABORATORY. Cold Spring Harbor Symposia on Quantitative Biology, Vol. 59. The molecular genetics of cancer; 59th Symposium on Quantitative Biology, Cold Spring Harbor, New York, USA, June 1-8, 1994. xxvii+739p. Cold Spring Harbor Laboratory Press: Plainview, New York, USA. ISBN 0-87969-068-2(paper); ISBN 0-87969-067-4(cloth).

ISSN: 0091-7451 Language: ENGLISH

Print Number: Biological Abstracts/RRM Vol. 047 Iss. 009 Ref. 152164

16/7/11 (Item 11 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

11778798 BIOSIS Number: 98378798

Alterations in Notch signaling in neoplastic lesions of the human cervix Zagouras P; Stifani S; Blaumueller C M; Carcangiu M L; Artavanis-Tsakonas

Dep. Biol., Yale Univ., New Haven, CT 06536, USA

Proceedings of the National Academy of Sciences of the United States of America 92 (14). 1995. 6414-6418.

Full Journal Title: Proceedings of the National Academy of Sciences of the United States of America

ISSN: 0027-8424 Language: ENGLISH

Print Number: Biological Abstracts Vol. 100 Iss. 005 Ref. 070636

The development of cancer is a cellular process that reflects and is partly driven by alterations in cell determination. Mutations in various molecules responsible for cell determination have been identified as being oncogenic, but little is known about the involvement of normal cell fate-determining mechanisms in the oncogenic process. The Notch pathway defines an evolutionarily conserved, general cell interaction mechanism that controls fundamental aspects of cell determination during vertebrate and invertebrate development. We have explored the involvement of the human Notch pathway in human cervical tissues, which define a cellular environment where cell fate changes take place and where neoplastic conditions have been well characterized. Our evidence suggests that Notch expression is associated with cell populations that are undergoing cell

fate changes and that Notch activity can be used to monitor cell fate abnormalities in cervical as well as other epithelial neoplasias.

16/7/12 (Item 12 from file: 5) DIALOG(R)File 5:BIOSIS PREVIEWS(R) (c) 1996 BIOSIS. All rts. reserv.

11572298 BIOSIS Number: 98172298

Drosophila in cancer research: The first fifty tumor suppressor genes Watson K L; Justice R W; Bryant P J

Dep. Molecular Cellular Biol., Harvard Univ., Cambridge, MA 02138, USA Journal of Cell Science 0 (SUPPL. 18). 1994. 19-33.

Full Journal Title: Journal of Cell Science

ISSN: 0021-9533 Language: ENGLISH

Print Number: Biological Abstracts Vol. 099 Iss. 008 Ref. 112601 Print Number: Biological Abstracts/RRM Vol. 047 Iss. 005 Ref. 069789

Drosophila, over 50 genes have been identified in which loss-of-function mutations lead to excess cell proliferation in the embryo, in the central nervous system, imaginal discs or hematopoietic organs of the larva, or in the adult gonads. Twenty-two of these genes have been cloned and characterized at the molecular level, and nine of them show clear homology to mammalian genes. Most of these mammalian genes had not been previously implicated in cell proliferation control. Overgrowth in some of the mutants involves conversion to a cell type that, in normal development, shows more cell proliferation than the original cell type. Thus the neurogenic mutants, including Notch, show conversion of epidermal cells to neuroblasts, leading to the 'neurogenic' phenotype of excess nervous tissue. The ovarian tumor mutants show conversion of the female germ line to a cell type resembling the male germ line, which undergoes more proliferation than the female germ line. Mutations of the fat locus cause hyperplastic overgrowth of imaginal discs, in which the epithelial structure is largely intact. The predicted fat protein product is a giant relative of cadherins, supporting indications from human cancer that cadherins play an important role in tumor suppression. Mutations in the lethal(2)giant larvae and lethal(1)discs large genes cause neoplastic overgrowth of imaginal discs as well as the larval brain. The dig gene encodes a membrane-associated quanylate kinase homolog that is localized at septate junctions between epithelial cells. This protein is a member of a family of homologs that also includes two proteins found at mammalian tight junctions (ZO-1 and ZO-2) and a protein found at mammalian synaptic junctions (PSD-95/SAP90). Genes in which mutations cause blood cell overproduction include aberrant immune response-8, which encodes the RpS6 ribosomal protein and hopscotch, which encodes a putative non-receptor protein tyrosine kinase. The gene products identified by ovarian tumor mutants do not show clear amino acid sequence homology to known proteins. Drosophila provides an opportunity to rapidly identify and characterize tumor suppressor genes, many of which have mammalian homologs that might also be involved in cell proliferation control and tumor suppression.

16/7/14 (Item 14 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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11492147 BIOSIS Number: 98092147

The human NOTCH1, 2, and 3 genes are located at chromosome positions

9q34, 1p13-p11, and 19p13.2-p13.1 in regions of neoplasia-associated translocation

Larsson C; Lardelli M; White I; Lendahl U

Dep. Cell Mol. Biol., Med. Nobel Inst., Karolinska Hosp., S-171 77 Stockholm, Sweden

Genomics 24 (2). 1994. 253-258.

Full Journal Title: Genomics

ISSN: 0888-7543 Language: ENGLISH

Print Number: Biological Abstracts Vol. 099 Iss. 005 Ref. 062557

In Drosophila the Notch gene controls differentiation to various cell fates in many tissues. Three mammalian Notch homologs have recently been identified: Notch 1, 2, and 3. All three homologs are very highly conserved relative to the Drosophila Notch gene, which suggests that they are important for cell differentiation in mammals. This notion is supported by the previous finding of a truncated, translocated form of the human NOTCH1 gene (formerly TAN1) in three cases of leukemia. Given this genetic link between NOTCH1 and tumor formation, it is of interest to establish the chromosomal positions of the other two homologs. We report the identification of cosmid clones for the human NOTCH1, 2, and 3 genes. These clones were used as probes in fluorescence in situ hybridization to human metaphase chromosomes, and the results, combined with data from somatic cell hybrid panels, show that the NOTCH2 and 3 genes are located at positions 1p13-p11 and 19p13.2-p13.1, respectively, which are regions of neoplasia-associated translocation.

16/7/15 (Item 15 from file: 5) DIALOG(R)File 5:BIOSIS PREVIEWS(R) (c) 1996 BIOSIS. All rts. reserv.

11292950 BIOSIS Number: 97492950

An activated Notch suppresses neurogenesis and myogenesis but not gliogenesis in mammalian cells

Nye J S; Kopan R; Axel R

Dep. Neurol., Inst. Cancer Res., Coll. Physicans Surg., Columbia Univ., New York, NY 10032, USA

Development (Cambridge) 120 (9). 1994. 2421-2430.

Full Journal Title: Development (Cambridge)

ISSN: 0950-1991 Language: ENGLISH

Print Number: Biological Abstracts Vol. 098 Iss. 010 Ref. 128689

P19 cells, a mouse embryonal carcinoma line, can be induced to differentiate into neurons. After induction, however, only a small subpopulation of cells develop as neurons, suggesting that equipotent cells adopt different cell fates. In invertebrate systems, the lin-12-Notch family of genes is thought to control the choice of cell fate. We have therefore asked whether activation of murine Notch (mNotch) regulates neuronal differentiation in P19 cells. We demonstrate that a dominant gain-of-function mutant of mNotch suppresses neurogenesis, as well as myogenesis in P19 cells. Overexpression of the full-length mNotch protein also suppresses neurogenesis. In contrast, the differentiation of glia is not affected by an activated mNotch homologue. These data indicate that mNotch may play a central role in the choice of cell fate in differentiating cells in culture and suggests that mNotch may play a similar role in the choice of fate in the developing mammalian embryo.

16/7/17 (Item 17 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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11038694 BIOSIS Number: 97238694

A human homologue of the Drosophila developmental gene, Notch, is expressed in CD34+ hematopoietic precursors

Milner L A; Kopan R; Martin D I K; Bernstein I D

Fred Hutchinson Cancer Res. Cent., 1100 Fairview Ave. N, Seattle WA 98109, USA

Blood 83 (8). 1994. 2057-2062.

Full Journal Title: Blood

ISSN: 0006-4971 Language: ENGLISH

Print Number: Biological Abstracts Vol. 097 Iss. 011 Ref. 155807

Members of the Notch gene family have been shown to mediate cell-fate decisions by multipotent precursors in a number of different systems. To determine whether members of this family might play a similar role in hematopoiesis, we asked if homologues of the Notch gene are expressed in hematopoietic precursors. Using degenerate oligonucleotides corresponding to conserved amino acid sequences in known Notch homologues as primers for the polymerase chain reaction (PCR), we demonstrated that at least one Notch homologue is expressed in human bone marrow CD34+ cells, a population enriched for hematopoietic precursors. Cloning and sequencing of the PCR products identified this Notch homologue as TAN-1, a member of the Notch family previously cloned from a T-cell leukemia with a translocation involving this gene. Subsequent evaluation of bone marrow hematopoietic cells for TAN-1 expression using a reverse transcription-PCR assay confirmed the expression of TAN-1 in CD34+ hematopoietic precursors, including the immature subset that lacks expression of lineage-associated antigens (CD34+lin-). These findings, together with the known role of Notch homologues in other systems, suggest that members of the Notch family, included TAN-1, may be involved in mediating cell-fate decisions during hemotopoiesis.

16/7/23 (Item 23 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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9139819 BIOSIS Number: 93124819

EXPRESSION OF AN ACTIVATED NOTCH-RELATED INT-3 TRANSGENE INTERFERES WITH CELL DIFFERENTIATION AND INDUCES NEOPLASTIC TRANSFORMATION IN MAMMARY AND SALIVARY GLANDS

JHAPPAN C; GALLAHAN D; STAHLE C; CHU E; SMITH G H; MERLINO G; CALLAHAN R LAB. MOLECULAR BIOL., NATL. CANCER INST., NATL. INST. HEALTH. BETHESDA, MD. 20892, USA.

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Expression of the int-3 locus is activated in mouse mammary tumors as a consequence of insertional mutagenesis by the mouse mammary tumor virus (MMTV). Integration of the MMTV provirus into the into-3 locus promotes the transcription and translation of flanking cellular int-3 sequences sharing significant homology with the intracellular domain of the nuerogenic Notch gene of Drosophila, and with the yeast cell cycle regulatory genes cdc10 and SW16. To determine the in vivo consequences of activated int-3 expression, transgenic mice were generated harboring a genomic tumor DNA

fragment consisting of the MMTV LTR and the flanking cellular int-3 sequences. All six int-3 founder transgenic mice and the progeny of one established line exhibited similar dramatic phenotypic abnormalities in tissues in which the transgene was expressed. Focal and often multiple poorly differentiated mammary and salivary adenocarcinomas appeared in the majority of transgenic mice between 2 and 7 months of age. Significantly, mammary glands were arrested in development and were lactation deficient in all female int-3 mice. The salivary glands, glands of the nasal mucosa and maxillary sinus, the extraorbital lacrimal glands, and the Harderian glands of juvenile and adult transgenic mice all contained proliferating immature ductule cells and were incompletely differentiated. In addition, all male int-3 transgenic mice were sterile, apparently the result of severe hyperplasia of the epididmyis. These findings demonstrate in vivo that expression of the activated Notch-related int-3 gene causes deregulation of developmental controls and hyperproliferation of glandular epithelia.

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DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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TAN-1 THE HUMAN HOMOLOG OF THE DROSOPHILA NOTCH GENE IS BROKEN BY CHROMOSOMAL TRANSLOCATIONS IN T LYMPHOBLASTIC NEOPLASMS

ELLISEN L W; BIRD J; WEST D C; SORENG A L; REYNOLDS T C; SMITH S D; SKLAR

STANFORD UNIV. SCH. MED., STANFORD, CALIF. 94305.

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Previously we described joining of DNA in the .beta. T cell receptor gene to DNA of an uncharacterized locus in a $t(7;9)\,(q34;q34.3)$ chromosomal translocation from a case of human lymphoblastic leukemia (T-ALL). We now show that the locus on chromosome 9 contains a gene highly homologous to the Drosophila gene Notch. Transcripts of the human gene, for which we propose the name TAN-1, and its murine counterpart are present in many normal human fetal and adult mouse tissues, but are most abundant in lymphoid tissues. In $t(7;9)\,(q34;q34.3)$ translocations from three cases of T-ALL, the breakpoints occur within 100 bp of an intron in TAN-1, resulting in truncation of TAN-1 transcripts. These observations suggest that TAN-1 may be important for normal lymphocyte function and that alteration of TAN-1 may play a role in the pathogenesis of some T cell neoplasms.

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DIALOG(R)File 73:EMBASE
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T cell leukemia-associated human Notch/translocation-associated Notch homologue has IkappaB-like activity and physically interacts with nuclear factor-kappaB proteins in T cells

Guan E.; Wang J.; Laborda J.; Norcross M.; Baeuerle P.A.; Hoffman T. Division of Monoclonal Antibodies, Federal Drug Administration, Ctr. for Biologics Evaluation/Res., 8800 Rockville Pike, Bethesda, MD 20892 USA Journal of Experimental Medicine (USA), 1996, 183/5 (2025-2032) CODEN: JEMEA ISSN: 0022-1007

LANGUAGES: English SUMMARY LANGUAGES: English

Translocation-associated Notch homologue (TAN-1), a gene originally cloned from the translocation breakpoint of a human T cell leukemia carrying a 9:7(q34.3) translocation, encodes a protein belonging to the Notch/Lin- 12/Glp-1 receptor family. These receptors mediate the specification of numerous cull fates during development in invertebrates and vertebrates. The intracellular portion of Notch/TAN-1 contains six ankyrin repeats that are similar to those found in cytoplasmic IkappaB proteins. IkappaB proteins are specific inhibitors of nuclear factor (NF)-kappaB/Rel transcription factors. Here we show that TAN-1 has functional properties of an IkappaB-like regulator with specificity for the NF-kappaB p50 subunit. A recombinant polypeptide corresponding to the cytoplasmic portion of TAN-1 (TAN-1(C)) specifically inhibited the DNA binding of p50-containing NF-kappaB complexes. When overexpressed in an appropriate cell line, TAN-1(C) prevented kappaB-dependent transactivation in transient reporter gene assays in a fashion similar to the structurally related protein, Bcl-3. TAN-1(C) could activate kappaB-dependent gene expression by attenuating the inhibitory effect of an excess of p50 homodimers. Immunoprecipitation experiments showed that the TAN-1 from a T cell line is associated with NF-kappaB containing p50 and p65 subunits. These observations indicate that TAN-1(C) may directly engage NF-kappaB transcription factors and modulate nuclear gene expression. ?LOGOFF